



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 111055

TO: Jeffrey Parkin
Location: cm1/8e15/8e12
Art Unit: 1648
Friday, January 02, 2004

Case Serial Number: 08/573569

From: Toby Port
Location: Biotech-Chem Library
CM1-6A04
Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Parkin,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

STIC-Biotech/ChemLib

CRFE

111055

From: Parkin, Jeffrey
Sent: Friday, December 26, 2003 8:18 PM
To: STIC-Biotech/ChemLib
Subject: U.S. Serial No. 08/573,569

Please search **SEQ ID NO 15** from **08/573,569** (Maassab, H. F., et al.) v. all relevant databases, including interference. Place results on both paper and disk. Thanks!

JSP
Au 1648
CM01-8E15
308-2227

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:31:30 ; Search time 8369 Seconds

(without alignments)
11443.355 Million cell updates/sec

Title: US-08-573-569-15

Perfect score: 2341
Sequence: 1 ACGGAGAGACGUCAUUUV.....AAAACGACCUUUCUACU 2341

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2886711 seqs, 2045481386 residues

1 number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_scs: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: gb_vl: *
16: em_ba: *
17: em_fun: *
18: em_hum: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_scs: *
28: em_un: *
29: em_vi: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pin: *
35: em_hcg_rod: *
36: em_hcg_mam: *
37: em_hcg_vrt: *
38: em_sy: *
39: em_hcgo_hum: *
40: em_hcgo_mus: *
41: em_hcgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2325	99.3	2341	14 FLAPB2A	M23970 Influenza A
2	2313.8	98.8	2341	14 FLAPB2PRO	M81575 Influenza A
3	2312.2	98.8	2341	14 FLAPB2PROA	M81581 Influenza A
4	2309	98.6	2341	6 AX399724	AX399724 Sequence
5	2309	98.6	2341	6 FLAPB2PROB	M81587 Influenza A
6	2305.8	98.5	2341	14 FLAH2NP2A	M73521 Influenza A
7	2332.2	95.4	2341	14 FLAH2NP2B	M73524 Influenza A
8	2217.8	94.7	2341	14 IAPB247	X99053 Influenza A
9	2213	94.5	2341	14 IAPB247MA	X99056 Influenza A
10	2191.4	93.6	2329	14 FLAPB2B	M91713 Influenza A
11	2184.2	93.3	2341	14 FLAP3MOA	J02140 Influenza A
12	2182.6	93.2	2341	14 INAS64804	AJ564804 Influenza
13	2173	92.8	2341	6 AX350184	AX350184 Sequence
14	2167.4	92.6	2329	14 FLAP2A	M91712 Influenza A
15	2159.4	92.2	2313	14 AF348170	AF348170 Influenza A
16	2156.2	92.1	2313	14 AF348171	AF348171 Influenza A
17	2129.8	91.0	2341	14 FLAPB2L	M38277 Influenza A
18	2115.4	90.4	2341	14 INFLX1	V00603 Influenza A
19	2113.8	90.3	2341	14 AF389115	AF389115 Influenza A
20	2110.6	90.2	2341	14 AB036782	AB036782 Influenza A
21	2110	90.1	2302	14 AF251394	AF251394 Influenza A
22	2104.2	89.9	2341	14 FLAP2CHILE	M27684 Influenza A
23	2104.2	89.9	2341	14 ORINPB2	X15283 Influenza A
24	2099.4	89.7	2341	14 IAU62543	U62543 Influenza A
25	2096.2	89.5	2341	14 AF258842	AF258842 Influenza A
26	2088.2	89.2	2341	14 FLAP3M	J02179 Influenza A
27	2086.6	89.1	2341	14 FLAH3NP2	M73517 Influenza A
28	2077	88.7	2341	14 INAS64805	AJ564805 Influenza A
29	2043.4	87.3	2341	14 AF258524	AF258524 Influenza A
30	2038.6	87.1	2341	14 AF258841	AF258841 Influenza A
31	2033.8	86.9	2341	14 AF258525	AF258525 Influenza A
32	2028.8	86.7	2280	14 AF037412	AF037412 Influenza A
33	2028.8	86.7	2311	14 AF251402	AF251402 Influenza A
34	2025.6	86.5	2280	14 IAU71132	U71132 Influenza A
35	2024	86.5	2280	14 IAU71134	U71134 Influenza A
36	2020.8	86.3	2280	14 IAU71135	U71135 Influenza A
37	2019.2	86.3	2280	14 AF483602	AF483602 Influenza A
38	2014.4	86.0	2280	14 AF037413	AF037413 Influenza A
39	2009.6	85.8	2280	14 AF225514	AF225514 Influenza A
40	2006.6	85.8	2280	14 IAU71133	U71133 Influenza A
41	2006.4	85.7	2280	14 AF037414	AF037414 Influenza A
42	2006.4	85.7	2280	14 AF037415	AF037415 Influenza A
43	2006.4	85.7	2280	14 AF037416	AF037416 Influenza A
44	2006.4	85.7	2280	14 AF225516	AF225516 Influenza A
45	2004.8	85.6	2280	14 AF225515	AF225515 Influenza A

ALIGNMENTS

RESULT 1
LOCUS FLAPB2A 2341 bp ss-RNA linear VRL 02-AUG-1993
DEFINITION Influenza A/Ann Arbor/6/60(H2N2) polymerase basic 2 protein (PB2), segment 1) RNA, complete cds.
ACCESSION M23970 J04349 M23971
VERSION M23970.1 GI:324981
KEYWORDS polymerase; polymerase basic 2.
SOURCE Influenza A virus
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.
REFERENCE 1 (bases 1 to 2341)
AUTHORS Cox,N.J., Kilame,F., Kendal,A.P., Maassab,H.F. and Naeye,C.
TITLE Identification of sequence changes in the cold-adapted, live

D	121	AAAGAGTACACTCAGGGAGACAGAAAAAGAACCCGTCACTTAGATGAATGATGATG	180
Q	181	GCATUAAUAUUCGGAUUDACAGCCGACAAAGAGUAUACAAUAUAGUUCCTGAGAAUAU	240
D	181	GCATGAAGAAATATCCGATTCACCTGACAAAGAGATPAACAGAAATGATTCCTGAGAGAAAT	240
Q	241	GAGCAAGGGCAAACTUCUATUGAGUAAAUAAGATUAGUCCCGAUCGGAUCGUAUGUUA	300
D	241	GAGCAAGGGCAAACTTATGAGAGTAAATGAGATGATGCGAGATCGAATGAGATGAGTA	300
Q	301	UCACUCUCUGCUGUGACAUUGAGUGAAUUAAGAAUUGACCAUUGACCAUAGACGUGUAU	360
D	301	TCACCTCTGCGCTGTGACATGTGTGGAATGAAATGACCAATACATACATACGTTCAATAT	360
Q	361	CCAAAUUCUACAAAUCUUAUUGAGAAAGUGCGAAAGGUAUAAAUAUGAACCTUUGGC	420
D	361	CCAAAUATCTACAAAACCTTATTTGAGAAAGTCGAAAGGTTAAACATGGAACCTTTGGC	420
Q	421	CCUGUCCAUUUUAGAAACCAAUCAAAUAAGCCCGAAGAGUGUACUAUAUUCUGUCU	480
D	421	CCUGUCCAUUUUAGAAACCAAUCAAAUAAGCCCGAAGAGUGUACUAUAUUCUGUCU	480
Q	481	GCAGACUCUACUGUCCAAAGAGGACACAGAGUUAUAUUGAAAGUUGUUUUCUUAACGA	540
D	481	GCAGACCTCAATGTCGCAAGGAGGACACAGATGTAAATCAATGAAATGTGTTTCCCTAACGA	540
Q	541	GUGGGGGCCAGGUAUCUACGUCGAGUUCGCAUUAUACAUAUCCAAAGAGAAAAAGAA	600
D	541	GUGGGGGCCAGGATTAACGTCGGAATTCGCAATTAACAATACAAAGAGAAAAAGAA	600
Q	601	GACUCCGAGAUUGCAAAUUAUUCACCUUUGAGUGUGGUAUCUGUAAGAGAGACUU	660
D	601	GAACTCCAGAGATTCGAAAAATTTCTCCTTGAATGTTGGTACATGTTAGAGAGAACCTT	660
Q	661	GUCCGAAAAAGAAUUAUUCUCCAGUUGCUGUGUGAAACAAGAGUGUAUUAUUGAACUG	720
D	661	GUCCGAAAAAGAGAAATTTCTCCAGATGTGTGATGGAACAAGAGTGTATCAATTTGAATGT	720
Q	721	UUGCACUUGACUCACAAAGAACAUGCUGUGGAAACAAGUUAACUCCGAGUGGAGAAUGAG	780
D	721	TTGCACTTGACTCAAGAAACATGCTGGGAAACAGATGTACACTCCAGGTTGGAAGTGAAG	780
Q	781	AAUGCAUGUUGUUAUUAUUGUAGUUAUUAUUGCAGCCAGAGCAUAUGUGAAAGACACA	840
D	781	AATGATGATGTTGATCAAAAGTCTAATTTTCAGACGACAGAACATGTAGAAAGACACA	840
Q	841	GUAUDAGAGAUCCACUAGCAUUCUUUUGAGAGUUGCCACAGACACAGAUUGGCGGG	900
D	841	GTATCAGAGATCCACTAGACATCTTATTTAGAGATGTGCAACAGACAACAATTTGGCCGG	900
Q	901	ACAAAGAUUGUGACAUUCUUGAGCAGAAACCAACAGAAAGACAGUGUGAAUAUUGC	960
D	901	ACAAAGATGTGTGACATTTCTTAGCGAGAAACCAACGAAAGACAGCTGTGATATATGC	960
Q	961	AAAGCUGCAUUGGACUAGAGAUACGUCUACUUACAUUUUGGCGGGUUCACAUUUAG	1020
D	961	AAAGCTGCAATGCGACTGAGAAATCAGCTCATCTTCAGTTTGGGGGTTTCACATTTAAG	1020
Q	1021	AGAACAAACCGAUUCUACUAGUCACAGAGAGAGAAAGAAUUGUCUACCGGCAUUCUCAA	1080
D	1021	AGAACAAACCGATCTCACTCAAGTCAAGAGAGAGAAAGAAAGTCTTAACGGCAATCTTCAAA	1080
Q	1081	UTGAAAAAAGAGGUGUACUAGAGGAAAGACAGAGUUCACAUUGUGUGGAAAAAGGCAACA	1140
D	1081	TTGAAAAATTAAGGTGTCATGAGGATTAACAGAGAGTTCAACATGTGTTGGAAAAAGGCAACA	1140
Q	1141	GCUAUAUCUACAAAAAGCAACCGAGAUUUGAUUACUGUACUGUAGUGAGAGACCAA	1200
D	1141	GCTATACTCAGAAAAAGCAACCGAGAGATTGATTCAGCTGATGTGATGTGAAGACGAA	1200
Q	1201	CAGUCGUAUGCUGAAAGCAUAUAUUGUGGCCACUGUAUUUUUACAAGAAAGUUGUAUGUA	1260
D	1201	CAGTCGATAGCCGAAGCAATAATTTGTGCCATGAGTAATTTTCAAGAAAGATTGTATGATA	1260

QY	1261	AAAGAGTUNAGAGGUGUACUAAUUTUGGUAUUGGGCCAAUUCAGCGCAUUGAACCCAAU	1320
Db	1261	AAAGGAGTTAAAGGATGATCTGAATTTGCTTAATAGGGCAAAATCAAGCAATGGAATCCAAATG	1320
QY	1321	CAUACAUCUUTUUAACAUAUUTUCAGAAAGAUUGCAGAAUGUCUUTUUCAAAUUTGGGGAAU	1380
Db	1321	CATCAACCTTTAAACAATTTTCAAGAGGATGCGAAAGATGCTTTTCAAAATTTGGGAATT	1380
QY	1361	GAACAUUUCGCAAUUGUGAUGGGAUUGAUTGGGUAUUAACAAGATGACUCCAGCAACA	1440
Db	1361	GAACATATCCGCAATATGGAATGGGAATATATGGGGATTATTAACAGCAATGACATCCAAAGACA	1440
QY	1441	GAGAUUGCAUAGAGAGGGGUAAAGAGUACGCAAAUUGGCGGUAUGAUAUACUCACAGCGG	1500
Db	1441	GAAGATTCMAATGAGAGGGGTAAAGATCAAGCAAAATGGGGCTGAATGAATATCTCAAGCGCG	1500
QY	1501	GAGAGAGUAGUGUGAGCAUUGACCGGUAUUTUGAGAUUCGAGCCAAACGAGAAUUGUA	1560
Db	1501	GAGAGAGTAAAGTGGAGACATTTGACCGGTTTGTAGAGATTCGAGCCAAACGAGGAAATGTA	1560
QY	1561	CUACUAUUCUCUGAGGAGUACUGUGAAACAAGGGAACAGAGAAACUGACAUAAUCUAC	1620
Db	1561	CTATTATCTCCTGAGAGAGTCAGTGAACACAGGGAACAGAGAACTGAACATATCTTAC	1620
QY	1621	UCAUCUGCAUAGAGUGUGGAGAUUAAUGGCGCUGAGUCAGUGUUGGUCUAUACCUACAG	1680
Db	1621	TCATGTCTAAATGATGTGGAGATTAAATGGCCCTGATCAAGTGTGGTCAATATCTTACAG	1680
QY	1681	UGGAUACAUCAGAAACUGGGAACUGUUAUAAUUCAGUGUCUCGAUUCUACAUAUCUA	1740
Db	1681	TGGATTCATCAAGAAACTGGGAAACGTTAAATTCAGTGGCTCGAAGATCCTTACATCTTA	1740
QY	1741	UACAUAUAAUAGGAUUTUGAGGCCUUAUCAGUCUUAUGUCUUAAGGCCAUUAGAGGCCAA	1800
Db	1741	TACATATAAATGGAATTTGAGCCATTTCAAGTCTTAACTTAAAGCCATTTAGAGGCCAA	1800
QY	1801	UACAGUGGUGUUTUGUAGGACUCUUAUUCCAACAAUAGGAGUUGAUCUUGGGACAUUTUGAU	1860
Db	1801	TACAGTGGGTTGTTAGGACTCTTATTCCAACAAATGAGGAGTATGATCTTGGGACATTTGAT	1860
QY	1861	ACCAACCCAGAUAAUAAACUUCUCCUUCGACGCGGCCCCCAAGAAAGCAAAAGUAUAUG	1920
Db	1861	ACCAACCCAGATAAATAAACTTCTTCCCTTGACACCGCCCAACAAAGCAAAAGTAGAATG	1920
QY	1921	CAGUUCUCUCACUGACUCUGAUAUGUGAGGGGAUCAGAAUAGAGAAUAUCUUGUAAGGGC	1980
Db	1921	CAGTTCTCTTCAATTTGACTGTGAATGTGAGGGGATCAAGAAATGAGAAATTACTGTAAAGGGC	1980
QY	1981	AAUUCUCUUAUUAUCAAACUACACAAAGCCACUAAAGAGACUAAACAUUCUCGAAAGAGU	2040
Db	1981	AAATCTCTCTGATTAATCACTACAAACAAACCACTAAGAGACTTAACAAATTTCTCGAAAGAT	2040
QY	2041	GCUGGACCUUUAUCUAGAAAGCCAGAGUAAAGGCAUUCUGGAGGUGAGUUCGCGUGUUCG	2100
Db	2041	GCTGGCACTTTAACTGAAAGACCCAGATGAAAGGACATCTTGAATGAGAGTCCGCTGTTCTG	2100
QY	2101	AGAGAGUUCUCUAUUCUGGGCAAAAGAAUGAUAAGGAUAUGGACCAAGCAUUAAGCAUCAU	2160
Db	2101	AGAGAGATTCCTCATTTCTGGCGAAAGAAAGATATGGAATATGGAACAGCATTTAAAGCATCAAT	2160
QY	2161	GAACTUGAGUAAACUUGCGAAAGGAAAGGUAUUGAUAUUAUUGGGCAAGGAGACGUG	2220
Db	2161	GAACCTGAGTAACCTTTGCAAAAGGAAAGGCTAATGACTAATTTGGGCAAGGAGACGTG	2220
QY	2221	GUGUUGCAUAGAAACGAAACGGAACUCUAGCAUACUUAUCUGACAGCCAGACAGCAACC	2280
Db	2221	GTTGTTGGTAATGAAGAACGAAACGGGACCTTATGCACTTAATGACAGCAGACGCGACC	2280
QY	2281	AAAAAGAUUCGGAUUGGCCAUCAUAUAUUGUUGAAUAAGUUTUAAAAAGCAACUUGUUTUCAG	2340
Db	2281	AAAAAGATTCGAGATGGCCATCAATTAATATGTCGAATAGCTTTAAAAAGCAACCTTGTCTTAC	2340

DB	2341 T 2341
RESULT 3 FLAPB2PROA	2341 bp ss-RNA linear VRL 12-FEB-2001
LOCUS	Influenza virus type A/Leningrad/134/17/57 (H2N2) PB2 gene,
DEFINITION	complete cds.
ACCESSION	M81581.2 GI:8281025
VERSION	
SOURCE	
ORGANISM	
REFERENCE AUTHORS	Influenza A virus (A/Leningrad/134/17/57 (H2N2)) Influenza A virus (A/Leningrad/134/17/57 (H2N2)) Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A; Influenza A virus; H2N2 subtype. 1 (bases 1 to 2341) Klimov,A.I., Cox,N.J., Yotlov,W.V., Rocha,E., Alexandrova,G.I. and Kendal,A.P.
TITLE	Sequence changes in the live attenuated, cold-adapted variants of influenza A/Leningrad/134/57 (H2N2) virus
JOURNAL	Virology 186 (2), 795-797 (1992)
MEDLINE	92124758
PUBMED	1733114
REFERENCE	2 (bases 1 to 2341)
AUTHORS	Klimov,A.I.
JOURNAL	Direct Submission
TITLE	Submitted (20-JAN-1992) Research Institute for Viral Preparations, Academy of Medical Sciences of the USSR, Moscow, USSR
REFERENCE	3 (bases 1 to 2341)
AUTHORS	Klimov,A.I.
JOURNAL	Direct Submission
TITLE	Submitted (06-JUN-2000) Influenza Branch, G-16, Centers for Disease Control and Prevention, 1600 Clifton Rd., Atlanta, GA 30333, USA
REMARK	Sequence updated by submitter
COMMENT	On Jun 6, 2000 this sequence version replaced gi:324997.
FEATURES	Location/Qualifiers
source	1..2341
gene	/organism="Influenza A virus (A/Leningrad/134/17/57 (H2N2))"
CDS	/mol_type="genomic RNA" /strain="A/Leningrad/134/17/57 (H2N2)" /db_xref="taxon:152281" 28..2307 /gene="PB2" 28..2307 /gene="PB2" /codon_start=1 /product="PB2 protein" /protein_id="AAI19214.2" /db_xref="GI:8281026"
BASE COUNT	797 a 415 c 586 g 543 t
ORIGIN	
Query Match	98.8%; Score 2312.2; DB 14; Length 2341;
Best Local Similarity	76.3%; Pred. No. 0;
Matches 1786; Conservative 537; Mismatches 18; Indels 0; Gaps 0;	

OY		1	AGCGAAACGACGUCUAUUUUNUGCAAUUGGAAAAGAAATAAAGAATCAAUCGGAATUCGAG	60
Dd		1	AGCAAAAGCGAAGCTCAATTATATTTCAATATGGAAAAAGAAAAGAACTACGAAATCTGATG	60
OY		61	UOSGAGUCUCCCAUCUCGCGAGAUACUAAACAAAACAAGUGGACCAUAUGGCCCUAAUUVU	120
Dd		61	TGGCAGTCTGCACCTCCGGAGACTCTAACAAAACACAGTGAGACCATATGCCCCATAATT	120
OY		121	AAGAAGUACAUCAUGGAGGCGAGAAAAGAACCCGfUCAUUAGAUAGAAUUGAVUG	180
Dd		121	AAGAAGTACACATCAGGAGGACAGAAAAAGAACCCGTCACTTAGAGTAATAATGATGTATG	180
OY		181	GCAUVGAUUUVCCGAUUUACGCCGACAAAGGAAUACAGAAUANGAUUUCUGAGGAANU	240
Dd		181	GCAATGAATATTCGATTTACAGCTGACAAAGGATTAACAGAAATGAATTCCTGAGAGAAAT	240
OY		241	GAGCAAGGGCAAAUCUUAUGGAGUAAAAUGAGUAVUGCCGAAUCCGAGUCGUGUGAUGVA	300
Dd		241	GAGCAAGGGCAAACTCTATGSAAGTAAATGAGTGAATGCCGATGGGATCGAGTGAATGTA	300
OY		301	UACACUCUGCUGUGACAUUGUGGAAUAGAAUUGAACCAUAGACAAAGUACGGUUCAUUV	360
Dd		301	TCACCTCTGGCTGTGACATGATGGAATVAGAAATGAGCAATAGAACAGTACGGTTCATTAT	360
OY		361	CCAAAAUUCUACAAAUCUUVUUUGAAGAAAGUCGAAAGSUVUAAAACAVGAAACCUUGGC	420
Dd		361	CCAAAAATCTACAAAACCTTATTTTGAAGAAAGTCCAAAGGTTTTAAACATVGAAACCTTTGCG	420
OY		421	CCUGUCCAUUUUAGAAACCAAGUCUAAAUAUCCGCCAAGAGUUGACUAAUAUCCUGUGUCU	480
Dd		421	CCTGTCCATTTTAAABACCAAGTCAAAATVAGCCGAAGAGTTGACATTAATCTGTGTCAT	480
OY		481	GCAGACCUCAGUGCCCAAGAGGCAACAGAGUUAUACUAGAAAGUUVUUUCCUUAACGA	540
Dd		481	GCACACCTCAGTGCACAAAGAGGACACAGATGTATCATAGAAAGTTTTCCTTAACGA	540
OY		541	GUGGGGGCCAGGAAUACUAAUCGUGGAAUCCGCAUUAACAAUAAACCAAGAAAAAGAA	600
Dd		541	GTVGGGGCCAGGAAATCTAACGTCCGAAATCCGCAATTAACAAATVAAACCAAGAAAAAGAA	600
OY		601	GAAUCUCCAGAGUCCAAAUUVUACACUUUGAGUUGUCUUAAGUUGAAGAGAAACUUV	660
Dd		601	GAACTCCAGAGTTCGAAAAATTTCTCTTTTATGAGTGGCATATGTTAGAAAGACACTT	660
OY		661	GUCCGAAAAACGAGAUUUCUCCAGUUGCUGUGUGGAAACAAACAGUGUUAUAUUAAGUG	720
Dd		661	GTCGAAAAACGAAATTTCTCCAGTTGCGTGTGGAAACAACATGTGTATCATTTGAAGTG	720
OY		721	UUGCACUUGACUCACAGAAACAUUGCUGGGAACAGAUUGUACACUCCAGUGUGGAAAGUGG	780
Dd		721	TTTGCACTTTGACTCAAGGAAACATGCTGGGAAACAGATGTATCACTCCAGGTGAGAAAGTGAG	780
OY		781	AUUGAUUGUUGAUUCAAAGUCUUAUUUUGCAGCCACAGGACUAUGAGAAAGACAGCA	840
Dd		781	AATATATATGTGTGATCAAAAGTCTAATTAATTGCAACCAGGAAACATATGTAGAAAGACACA	840
OY		841	GUATCAGCAGUCCACUAGCACUUCUUUUVUGAGAGUUGGCCACACACACAGAUUUGCGGG	900
Dd		841	GTAACACAGATTCACACTACGACTCTTTATTTGAGATGTGCCACACACACACAAATTTGGCCGG	900
OY		901	ACAAAGAUUGUGACAUUCUUAUGGACAGAACCCAACAGAAAGAACAGUUGGAAAUUAGC	960
Dd		901	ACAAAGATVTGGGCACTTTTATAGCAGAACCCAACGMAAGGCAAGCTGTGATATATATGC	960
OY		961	AAGGCTUGCAUUGGACUGAGAUAGCUCUACUCCUUCAGUUVUUGCGGGSUUCACAUUUAAG	1020
Dd		961	AAGGCTUGCAUUGGACUGGAAATACGATCACTCTTCAAGTTTGTGGCGGGTTTCACATTTTAAG	1020
OY		1021	AGAAACAAGCCGAGUACUAGUACAAAGAGAGAGAAAGAGUUGCUUAGGGGCAUUCUCAAACA	1080
Dd		1021	AGAAACAAGCCGATCATATAGTCTAAGAGAGAGAGAAAGTCTTACGGGCAATCTTCAAACA	1080
OY		1081	UUGAAAAUAAAGGUGCACUAGAGGACUACAGAGAGUUCACAAUUGSUUGGAAAAAGGCAACA	1140

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Db      1081 TTGAAATTAAGGTCATAGGAGATACAGAGAGTTCAACAATGTTGGGAAAAAGGCAACA 1140
Qy      1141 GCUAUAUCUAGAAAAAGCAACGAGAGUUGAUUCUGUCUGUUGUGAGUGAGAGACGA 1200
Db      1141 GCTATTAATCTCAGAAAAAGCAACGAGAGATTGATTTCAGATGATGAGTGAAGAGAGCA 1200
Qy      1201 CAGUGCAUUGCGUAGCAUAUAUUGUGGCGCAUGGUUUAUUCACAAAGAAUUGUUAUA 1260
Db      1201 CAGTGCATGCGCAAGCAATTAATTTGCGCATGTGATTTTCACAAGAAATTTGATATGA 1260
Qy      1261 AAAAGAGUAGAGUGUAGUUGUUAUUGGUAAAGGCGAAUACGCGAUUGUAGUCCG 1320
Db      1261 AAGAGAGTTAGAGGTGATCTGAATTTCTTAATAGGCAATCAAGCATGATGATCCATG 1320
Qy      1321 CAUCAAUUUUUUAAGCAUUUUUUCAGAGAGUAGGUAAGUGUUUUUUAUUUGGAGAAU 1380
Db      1321 CATCAACCTTTTAAGACATTTTTCAGAAAGATGCGAAAGTCTTTTCAAAATTTGGGAAAT 1380
Qy      1381 GAACAUUUCGACAAUUGUAGUGGAAUUGAUUGGCGUUAUCCAGACUAGACUUCGCAAGCA 1440
Db      1381 GAACATATCGACAAATGTGATGGGAAATGATYGGGATTTACAGACATGATCTCCAGACCA 1440
Qy      1441 GAGAGUUCUAGAGAGGCGUAAAGAGUCAGCAAAAUUGGCGUAGUAGUAAUACUCGAGCG 1500
Db      1441 GAGATGTCAATAGAGGCTTAAAGAGTCAACCAAAATGGCGCTAGATGAACTCCAGCGCG 1500
Qy      1501 GAGAGAGUAGUGUGAGCAUUGACCGGUUUUUGAGUUGUAGUAGUAGUAGUAGUAGU 1560
Db      1501 GAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Qy      1561 CUACUUAUUCUUCUAGAGAGUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1620
Db      1561 CTATTAATCTCTGAGAGAGCTCAGTGAACACAGGAGAAAGAGAACTGACATTAATCTTAC 1620
Qy      1621 UCAUUGGUGUAGUAGUGGAGUAGUUAUUGGCGUAGUAGUAGUAGUAGUAGUAGUAG 1680
Db      1621 TCATGTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Qy      1681 UGCAUUCUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db      1681 TGGATCATCAGAAACCTGGGAAACCTGTTAAATTTAGTGGTCTCAAAATCTTACATGCTA 1740
Qy      1741 UACAAUUAUUAUUGGAUUTUGAGCCAUUUCAGUCUUUUAUUGUAGUAGUAGUAGUAG 1800
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Qy      1801 UACAUUGGUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1860
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Qy      1861 ACCACCCAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1920
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Qy      1921 CAGUUCUUCUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1980
Db      1921 CAGTCTCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
Qy      1981 AAUUCUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2040
Db      1981 AATTTCTCTGATTTCACTAACAACAAGACCACTAAGAGCTTAACAATTTCTGGAAAGAT 2040
Qy      2041 GCUUGCACUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2100
Db      2041 GCTGGGACCTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
Qy      2101 AGAGAGUUCUUCUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 2160
Db      2101 AGAGAGATTCCTCAATCTCTGGGCAAAAGAGATAGAGATAGAGACCAAGCATTTAAGCTCAAT 2160
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Db      2161 GAACTAGTAACTTGGCAAGAGAGAAAGGCTAATGTAATTTGGGCAAGAGACGTG 2220
Qy      2221 GUGUGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2280
Db      2221 GTGTTGTATATGAAAGAAACCGGACTAGATCTACTGACAGGCAAGAGAGAGG 2280
Qy      2281 AAAAGAGUUGGUGGCGCAUUAUUAUUGUUAUUGUUAUUAUUAUUAUUAUUAU 2340
Db      2281 AAAAGAAATTTGGATGCGCATCAATTAATGTCGATAGTTTAAAGACACTTGTCTAC 2340
Qy      2341 U 2341
Db      2341 T 2341

RESULT 4
AX399724 2341 bp DNA linear PART 06-JUN-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Influenza A virus (STRAIN A/SINGAPORE/1/57)
Influenza A virus (STRAIN A/SINGAPORE/1/57)
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
A viruses; Influenzavirus A; Influenza A virus; unidentified
subtype.

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ORIGIN

Query Match 98.6%; Score 2309; DB 6; Length 2341;
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Matches 1784; Conservative 537; Mismatches 20; Indels 0; Gaps 0;

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Qy      301 UCAACUUGGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 360
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Qy      421 CCUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 480

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Db	541	GUGGGGGCCAGGATACTTAACGTCCGAAATGCAATTAAACAACCAAGAGAAAAAGAA	600
Qy	601	GAACTCCAGGAATGCAAAATTTCTCTTGAAGGTGGTAATATTAGAGAGAACTT	660
Db	601	GAACTCCAGGAATGCAAAATTTCTCTTGAAGGTGGTAATATTAGAGAGAACTT	660
Qy	661	GUCCGAAAAACAGAAUUCUCCAGUGUCUGUGGAAACAAGCAGUGUUUACAUAUG	720
Db	661	GUCCGAAAAACAGAAUUCUCCAGUGUCUGUGGAAACAAGCAGUGUUUACAUAUG	720
Qy	721	UUGCACTTAACTCAAGAAACATGCTGGGAAACAGATGTACACTCCAGGTGGAGAAAGTGA	780
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Db	841	GUAAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUG	900
Qy	901	ACAAGAGUUGUGGAGACAUUCUUUGGAGAAACCAACAAGAAAGACAGUCUGUGAAUAGC	960
Db	901	ACAAGAGUUGUGGAGACAUUCUUUGGAGAAACCAACAAGAAAGACAGUCUGUGAAUAGC	960
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Db	961	AAAGCUGCAUUGGAGACUAGAGAUACAGCUCUACUAGUUUGCGGGUUUACAUAUAG	1020
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Db	1141	GCUAUACUCAGAAAACCAACGAGAGAUUAGUUGCUGCUAUGUGAGUGGAAAGACGA	1200
Qy	1201	CAGUGCAUUGCUGAAGCAUUAUUGGCAUUGGCAUUGUACAAGAAUATGUUACUA	1260
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Qy	1261	AAAGCAGUAGAGUGAUCUAGAUUUUGCUUAAUAGGCGAAAAUCAGCAUUGAUCUCCAU	1320
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Qy	1321	CAUCAAUUUAAAGCAUUAUUGCAGAAAGUCCGAAAGUGCUUUUUCAAAUUGGCGAAU	1380
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Qy	1381	GAAACUUAUACCAUUGUAGGAAUUGUUGGCAUUGGCAUUGUACAAGCAUUGCAUACCA	1440
Db	1381	GAAACUUAUACCAUUGUAGGAAUUGUUGGCAUUGGCAUUGUACAAGCAUUGCAUACCA	1440
Qy	1441	GAGAGUACAUAGAGAGCGGUAAAGAGUACCAAAUUGGCGGUAGUAGUACUCCAGCGCG	1500
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Qy	1501	GAGAGAGUAGUGGAGAGCAUUGACCGGUGUUUUGAGAGUUCAGAGCAACGAGAAUUGUA	1560
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REFERENCE	subType.
AUTHORS	1 Smeeht,C.A., Wright,K.E., Burns,B.F., Thaker,A.J. and Brown,E.G.
TITLE	Mutations in the hemagglutinin and matrix genes of a virulent influenza virus variant, A/Fw/1/47-WA, control different stages in pathogenesis
JOURNAL	Virus Res. 44 (2), 79-95 (1996)
MEDLINE	97033391
PUBMED	8879138
REFERENCE	2 (bases 1 to 2341)
AUTHORS	Brown,E.G.
TITLE	Direct Submission
JOURNAL	Submitted (03-JUL-1996) E.G. Brown, University of Ottawa, Dept of Microbiology & Immunology-Faculty of Medicine, 451 Smyth Rd, Ottawa Ontario K1H 8M5, CANADA
FEATURES	Location/Qualifiers
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BASE COUNT	797 a 420 c 584 g 540 t
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1	AAGAGTACACCTCAGAAAGACAGGAGAAAGAACCGTCACTTAGAGTAAATGATGATG 180
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Db      241 GAGCAAGGGCAAACTTTGTGAGTAAATGAAATATCCCGATCAAGCCAGATGATGTA 300
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Db      301 TCACCTCTGCGTGTGACATGGTGGATAGAAATGACCAATGACAAAGTACGGTTCAATTA 360
Qy      361 CCAAAAUCUACAAACUUAUUTUGAAGAAUGGAAAGGUAAAACUGGAAACCUUUGGC 420
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Qy      481 GCAGACCCUAGUGCCAAAGAGGCAACAGAUUGUAUUGAGAAUGUUGUUCUUAACGA 540
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Db      721 TTTCATTTGACTAGAGAACATGCTGGGAAACAGATTAACCTCAGGTGAGAGAAATGAG 780
Qy      781 AATGATGATGTGTATCAAAAGCCCTAAATTAATGCTGCCAGAGAACTATGTAAGAGATGTA 840
Db      781 AATGATGATGTGTATCAAAAGCCCTAAATTAATGCTGCCAGAGAACTATGTAAGAGATGTA 840
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Db      841 GTATCAGCAGATTCACATAGCATCTTATTTGAGATGTGCAACAGCACAGATTTGATG 900
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Qy      961 AAGGCGCAUUGGAGCUCAGAGAACACUACUCCUUAAGUUUGCGGUGUACAUUUAAG 1020
Db      961 AAGGCTGCAATGAGGACTGAGAAATCAGCTCAATCCTTCAATTTTCCGATTTCAATTTAG 1020
Qy      1021 AGAAACAGCGCAUCAGUACAGUACAGAGAGAGAAAGAGUGCCUUAACGGGCAAUUUAACA 1080
Db      1021 AGAAACAGCGGATCATCATGTCAGAGAGAGAGAGAAAGTCTTACGGGCAATCTTCAACA 1080
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Db      1081 TTGAAGATTAAGGCTGATGAGGAGTATGAAGAGTTTCACAATGCTTCCGAAAAAGGCAACA 1140
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Db      1381 GAACTATTCGACAAATGTGATGGGAATGATTTGGATATTAACAGACATGACCCCAAGACA 1440
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Db      1681 TGATCATCAGAACTGGGAAACGTTAATTAATTCAGTGTGTCAGAAATCTTACATGCTA 1740
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Db      1801 TACAGTGTGTTTGTAGAACTCTGTCCCAAAATGAGAGATGATGATGATGATGATGATGAT 1860
Qy      1861 ACCACCCAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1920
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Qy      1921 CAGUUCUUCUACUAGUACUGUAGUAGGGAUUCAGAAUUGAAUUAUUGUUAAGGCGC 1980
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IAPB247MA

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 Db 241 GGAACAACTCTATGAGTAAATGAGTGAATGCCGGGTGAGATCGAGTATGCTACCT 300
 QY 307 CUGGUGUGUAGUUGUGUAAUUGAACCAUAGACAGUACGUGUACUUAUUCACAAA 366
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 LOCUS

ACCESSION AX350184 GI:18615852
 VERSION AX350184.1
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 SOURCE ORANISM
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Db	1561	TTTACTATCTCTGAGGAGGTCAGGTGAAAC	CA	CAGGGGACAGAGAGACTGACATTAACCTTAC	1622	TTTACTATCTCTGAGGAGGTCAGGTGAAAC	CA	CAGGGGACAGAGAGACTGACATTAACCTTAC	1622	
Qy	1621	UCUACUCCUAAUGAUGUGGAGGAGUAUAU	UG	GGCCUUGAUGUCAGUGUGUCUAUUCUUAUCAG	1686	UCUACUCCUAAUGAUGUGGAGGAGUAUAU	UG	GGCCUUGAUGUCAGUGUGUCUAUUCUUAUCAG	1686	
Db	1621	TCATTCGTGCAATGATGTGGAGATTAATG	GC	CCCTGAGTCAAGTGTGTCAATTCATATCA	1686	TCATTCGTGCAATGATGTGGAGATTAATG	GC	CCCTGAGTCAAGTGTGTCAATTCATATCA	1686	
Qy	1681	UGGAAUACUACAGAAACUGGGAACUGUUA	AAU	UAUUGUCUUGUCUACAGUUCUUAUUGCUA	1746	UGGAAUACUACAGAAACUGGGAACUGUUA	AAU	UAUUGUCUUGUCUACAGUUCUUAUUGCUA	1746	
Db	1681	TGGATCATGACGAAACCTGGGAACCTGT	TA	ATAATTCATGGTCTCAGAAATCTCAATGT	1746	TGGATCATGACGAAACCTGGGAACCTGT	TA	ATAATTCATGGTCTCAGAAATCTCAATGT	1746	
Qy	1741	UACAAUAAAUAUGAAUUGAGCCAUUUC	AG	UCUUCUAGUCUUAAGUCCUAAAGGCCAUA	1800	UACAAUAAAUAUGAAUUGAGCCAUUUC	AG	UCUUCUAGUCUUAAGUCCUAAAGGCCAUA	1800	
Db	1741	TTCAACAAAATGGAATTTAGCCATTTCA	GT	CTTTAGTTGTTCTTAAGGCCATTAGAGCCAA	1800	TTCAACAAAATGGAATTTAGCCATTTCA	GT	CTTTAGTTGTTCTTAAGGCCATTAGAGCCAA	1800	
Qy	1801	UACAGUGGUGUUGUUGAGACUCUAUUC	CAA	AAUAGAGGAAUGUACUUGGACCAUUTUAC	1866	UACAGUGGUGUUGUUGAGACUCUAUUC	CAA	AAUAGAGGAAUGUACUUGGACCAUUTUAC	1866	
Db	1801	TTACAGTGGATTGTGCAAACTCTAATTC	CAA	AAATGAGGAAATGTAATTGAGCACTTTGAT	1866	TTACAGTGGATTGTGCAAACTCTAATTC	CAA	AAATGAGGAAATGTAATTGAGCACTTTGAT	1866	
Qy	1861	ACCACCCAGAUUAUAAAACUUCUUC	CCC	UUUGAGCGCCGCCCAACAAAGUUAUAUG	1920	ACCACCCAGAUUAUAAAACUUCUUC	CCC	UUUGAGCGCCGCCCAACAAAGUUAUAUG	1920	
Db	1861	ACCACCCAGATATATAAGCTTCCCTT	GC	AGCGGCCCAACAAAGATATATG	1920	ACCACCCAGATATATAAGCTTCCCTT	GC	AGCGGCCCAACAAAGATATATG	1920	
Qy	1921	CAGUUCUUCUACUCUAGUCUUAUUG	AG	GGGGAUCAGAAUAGAUACUUGUUAAGGGCC	1980	CAGUUCUUCUACUCUAGUCUUAUUG	AG	GGGGAUCAGAAUAGAUACUUGUUAAGGGCC	1980	
Db	1921	CAGTTCTCTTCAATGACCTGTGAAT	GT	GAGGGGATCAGGAGTAGAATATCTTGTAAGGGCC	1980	CAGTTCTCTTCAATGACCTGTGAAT	GT	GAGGGGATCAGGAGTAGAATATCTTGTAAGGGCC	1980	
Qy	1981	AAUUCUCCUAAUUAUUCACUACAACA	AG	ACCAACCAUUAAGACUUAUUCUGGAAAGG	2040	AAUUCUCCUAAUUAUUCACUACAACA	AG	ACCAACCAUUAAGACUUAUUCUGGAAAGG	2040	
Db	1981	ATTCTCTCTGTATTCACTACACAA	AG	ACCACCTTAATAAGCTTAACCTTCTG	2040	ATTCTCTCTGTATTCACTACACAA	AG	ACCACCTTAATAAGCTTAACCTTCTG	2040	
Qy	2041	GCUGGACACUUAUCUGAAGACCC	CAG	AUGAAGGCACAUUCUGAGUGGAGUCCG	2100	GCUGGACACUUAUCUGAAGACCC	CAG	AUGAAGGCACAUUCUGAGUGGAGUCCG	2100	
Db	2041	GCTGCACACTTTAATTAGGAAGCC	CA	GATGAAGCACATCCGAGTGAGATCCGCTGTTT	2100	GCTGCACACTTTAATTAGGAAGCC	CA	GATGAAGCACATCCGAGTGAGATCCGCTGTTT	2100	
Qy	2101	AGAGAAUUCUUCUACUCUGGCAAA	AG	AAAGAUAGAGAUUUGGACCAUUAAGCAU	2160	AGAGAAUUCUUCUACUCUGGCAAA	AG	AAAGAUAGAGAUUUGGACCAUUAAGCAU	2160	
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Qy	2221	GUGUUGUUAUAGAAACGAAACG	AA	CCGAAACUUCUACUUGCAGCGACAGC	2280	GUGUUGUUAUAGAAACGAAACG	AA	CCGAAACUUCUACUUGCAGCGACAGC	2280	
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Db	2341	T 2341				T 2341				
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DEFINITION	Influenza A/udorn/307/72 (H3N2), polymerase 2 (seg 1), RNA.									
ACCESSION	M91712									
VERSION	M91712.1									
KEYWORDS	GI:324901									
SOURCE	polymerase 2.									
ORGANISM	Influenza A virus									
REFERENCE	1 (bases 1 to 2329)									
AUTHORS	Lawson,C.M., Subbarao,E.K. and Murphy,B.R.									
TITLE	Nucleotide sequence changes in the polymerase basic protein 2 gene of temperature-sensitive mutants of influenza A virus									

Journal	Viriology	191 (1), 506-510 (1992)
MEDLINE	93033154	
PUBMED	1413525	
COMMENT	Original source text: Influenza virus type A (individual isolate A/udem/307/72) RNA.	
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BASE COUNT	788 a 415 c 585 g 541 t	
ORIGIN		
Query Match	92.6%; Score 2167.4; DB 14; Length 2329;	
Best Local Similarity	73.4%; Pred. No. 0;	
Matches 1709; Conservative 519; Mismatches 101; Indels 0; Gaps 0;		
Db	7 AGCAGGUCAAUUAUUAUGGAAAGAAUUAAGAUCUACGGAUUCUGAUGCCAG 66	
	1 AGCAGGTCATTTATTTACATATGGAAGATTAAGAACTACGGAATCTGATGTCCAG 60	
Qy	67 UCUCGCAUCUCCGAGAUACUAAACAAAACGACAGUGGACCAUUAUGCCCAUUAUAGAAG 126	
Db	61 TCTCGCACTCGCGAGATACTAACAAAACACACAGTGGACCATATGGCCATTAATTAAGAAG 120	
Qy	127 UACACAUACAGGAGCGACGAGAAAGAACCCGUCACUUGAUGAUAUGAUGAUGGCAUG 186	
Db	121 TACACATCAGGAGACAGAGAAAGAACCCGTTACTTAGATGAAGATGAGATGGCAATG 180	
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QY	547	GC	CGAGUACUAACUGCGGAUUGCCAAUUAACAUAUACCAAAGAGAAAAAGAAAGAACUC	606
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QY	607	CAG	AUUGCCAAAUUUAUACAUCUUAUUGGUGUGCUAUAUUGUUAAGAGAGAAUCUUGUCGA	666
Db	601	CAG	AUUGCCAAAUUUAUACAUCUUAUUGGUGUGCUAUAUUGUUAAGAGAGAAUCUUGUCGA	660
QY	667	AAAA	CGAGUUUUCUCCGAGUUGCGUGGAAACAAGCAGUGUGUAUAUUGAAGUGUGCAC	726
Db	661	AAAA	CGAGUATTTCTCCAGTTGCTGTGTGGAACAAGCAGTGTGTACATTTGAAGTTTACAC	720
QY	727	UUG	AUCUACAAGAACUUGUGGAAACAGUUAUAUCUACUGUGGAGAAAGUAGAAUUGU	786
Db	721	TTG	ACTCAAGGAAACGTGTGTGGAACAGATGTACCTCCAGGTGTGAAAGTGAATGAC	780
QY	787	GA	UGUUGUACAAAGUCUAUUAUUGCAGCCAGAGACUAGUGAAGAAAGCAGUUAUCA	846
Db	781	GA	UGUUGUACAAAGUCCTTAATTTTTCGAGCCAGAGAAATATGTGAAGAAAGCAGCATCA	840
QY	847	GC	AGAUCCACUAGCAUCUUAUUGGAGUUGGCCACAGCACAGAUUGCGCGGACAGG	906
Db	841	GC	AGATTCACATAGACATCTTTATTTGGAGATGTGCCACAGCACATGATTCGCGGACAGG	900
QY	907	AUG	UGUACAUUUCUUAAGCAGAAACCCACAAGAAAGCAAGUUGUGGAAAUUAUUGCAAGGCU	966
Db	901	ATG	TGTGGACATTTCTTTAGGCAGAACCCGACGAGAAACAAAGCTGTGTATATATGCAAGGCT	960
QY	967	GCA	UUGGACUUGAGGAGUUCAGUCUACUCUAGUUUGGCGGUGUACAUAUUAAGAGAAACA	1026
Db	961	GCA	UUGGAGCTGAGGATCAGCTCATCTTTCAGTTTGGTGGGTTCACATTTTAAGAGAAACA	1020
QY	1027	AG	CGAGUACUUCUGUACAGAGAGAGAGAAAGUUCUUAUGGCAUUCUUAACAUAUGAA	1086
Db	1021	AG	CGGCTCATCAATCAATAAAGAGAGAAAGATGTCTTAGCGGCAATCTTCAAAACATTGAA	1080
QY	1087	AUA	GGGUGUCCAGUAGGGAUACAGAGUUCACAAUUGUUGGAAAAGGGCAACAGCUUA	1146
Db	1081	ATA	AGGTGTCATGAGAGGGGTACAGAGATTCACAAATGATGTGGGAAAAGGGCAACAGCTATA	1140
QY	1147	CU	CAGAAAAAGCAACGAGGAGUUAUUCAGUCUAGUUUGAGUGGAGAGAGCAAGCAGUCG	1206
Db	1141	CTC	AGAAAAAGCAACGAGGATTTGGTTCACGCTTATATGTATGTGAAGGAGACAGACATCG	1200
QY	1207	AUA	GCUGAAGCAUAUAUUGGCGCAUUGGUUAUUCACAAAGAUUUGUUAUAAAAACA	1266
Db	1201	ATA	GCAGGAAGCGATATATTTACCATGTGTGTTTCCACAAGAGATTCATGATTAAGACA	1260
QY	1267	GU	UAGAGGUGAUCUGAAUUCGUUAUAUAGGCAUAUACGCAUUGCAUUCUCCAUUGCAUACA	1326
Db	1261	GTT	AGAGGTGACCTGAATTTCTGTAAACAGGGCAAAATCAGCGGTGTGAATCCCATGCATCA	1320
QY	1327	CU	UUAUAGCAUUAUUCACAAAGUCCGAAGUCUUUCAAATUUGGGGAAUUAUGAACAU	1386
Db	1321	CTT	TTTAAGCATTTTACAGAAAGATGCGAAAGTCTTTTCAGAAATTTGGGAAATTTGAACAT	1380
QY	1387	AUC	GCAUUGUAGUUAUUGGUGGUUAUACAGACAUUGCAUUCACAAGACACAGAGUUG	1446
Db	1381	ATC	GACAAATGTGTAGTGGAAATGTTTGAAGTATTTACAGACATACATCTCAAGCACAGAGATG	1440
QY	1447	UCA	UAGAGAGGGGUAAGAGUCACAAAUUGGGCGUAUGAUAUACUCCAGCGCGGAGACA	1506
Db	1441	TCA	ATAGAGGAATTAAGAGTCAAGCAAAATGGGCGTGAATGAAATCTCCAGCACAGAGAGG	1500
QY	1507	GU	UUGUGUGACUUGACCGGUGUUUUGAGAGUUCGAGCAACAGAGAAUUGUUAUACA	1566
Db	1501	GTA	GTGTGTTACATTTATCGGTTTTTGAGAGTTTCAGACCAACGTGGAATATATTACCA	1560
QY	1567	UUC	UCUAGAGGUGUACAGUAAACACAGGGAAACAGAAACUAGCAUAUAUCUACUACG	1626
Db	1561	TCT	CTCTGAGAGGTCACTGTAAACACAGGAAACAGAAACTGACATAAATCTTACCTATCG	1620

[illegible]


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FT      /+tag= d
XX      MO200224876-A2.
XX      28-MAR-2002.
XX      25-SEP-2001; 2001WO-EP11087.
XX      25-SEP-2000; 2000EP-0120896.
XX      (POLY-) POLYMER SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX      Kalinger H, Egorov A, Ferko B, Romanova J, Kalinger D,
XX      WPI: 2002-416282/44.
XX      P-PSDB; AAE23108.
XX      Manufacturing live vaccine, by infecting Vero cells with virus,
XX      combining cells with serum-free cell culture medium, incubating cells
XX      in presence of protease and nuclease, harvesting virus and preparing
XX      vaccine.
XX      Example 4; Page 38-39; 90pp; English.
XX      The present invention relates to a method for isolating viruses from
XX      various sources and for producing live attenuated influenza vaccines
XX      in a serum-free African green monkey kidney (Vero) cell culture under
XX      conditions where alterations in the surface antigens of the virus due
XX      to adaptive selection are minimised or prevented. The method is useful
XX      for the manufacture of whole-virus vaccine, preferably attenuated live
XX      vaccine. It is useful for prophylactic or therapeutic administration
XX      against viral infection, preferably influenza virus infections. The
XX      present sequence is Influenza A virus/singapore/1/57/cg (cold adapted)
XX      PB2 mutant cDNA. This sequence is used in the exemplification of the
XX      invention.
XX      Sequence 2341 BP; 798 A; 416 C; 585 G; 542 T; 0 other;
SQ      Query Match      98.6%; Score 2309; DB 24; Length 2341;
      Best Local Similarity 76.2%; Pred. No. 0;
      Matches 1784; Conservative 537; Mismatches 20; Indels 0; Gaps 0;
QY      1 AGCGAAGCAGGUCGUAUUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      1 AGCGAAGCAGGUCGUAUUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      61 UCGGAGUCUCCGACUCCGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      61 TCGGAGUCUCCGACUCCGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
QY      121 AAGAAAGUACACUUGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
DB      121 AAGAAAGUACACUUGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
QY      181 GCAUUAUAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      181 GCAUUAUAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      240 GCAUUAUAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      240 GCAUUAUAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      300 GAGCAAGGCGCAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      300 GAGCAAGGCGCAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      360 UCACUUGGAGUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      360 UCACUUGGAGUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      420 CCAAAAUUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      420 CCAAAAUUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      480 CCUGUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      480 CCUGUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG

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QY      540 GCAUUAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      540 GCAUUAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      600 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      600 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      660 GAAUUAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      660 GAAUUAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      720 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      720 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      780 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      780 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      840 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      840 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      900 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      900 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      960 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      960 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      1020 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      1020 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      1080 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      1080 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      1140 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      1140 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      1200 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      1200 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      1260 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      1260 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      1320 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      1320 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      1380 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      1380 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      1440 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      1440 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
QY      1500 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG
DB      1500 GUUGGAGGCGCAUUAUUGGAGUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUG

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QY 1561 CUACUUCUCUGAGAGAGUGACAGGAAACAGAGAAACUGACAUACUAC 1620
 DB 1561 CTACTATCTCTGAGAGAGTGAAGACAGAGAAACAGAGAACTGACATTACTTAC 1620
 QY 1621 UCAUCUGCAUAGUGUGGAGAUUAAUGCCUGAGUCAGUGUGUACUAAUACU 1680
 DB 1621 TCATCGTCAATGATGTGGAGATTAATGCCCCCTGATGATGTTGGTCACTTACTTAC 1680
 QY 1681 UGAUUCACAGAGAAACUGGAGAAACUGUUAUUAUUGAGUGUCAGAAUCCUACAU 1740
 DB 1681 TGGATCATCAGAAACTGGGAAACGTTTAAATTCAGTGTCTCAGAAATCCAGAAATGCTA 1740
 QY 1741 UACAAUAAUAGAAUUAUUGACCAUUAUUGAGUCUUAUUGAGGCAUUAAGGCGCA 1800
 DB 1741 TACATATAAATGAAATTTGAGCCATTTCACTTTAGTCTTAAAGCCATTAGAGCGCA 1800
 QY 1801 UACAGUGGUGUUGUAGAGACUCUUAUUCACAAUUGAGGAGUUAUCUGGAGACU 1860
 DB 1801 TACAGTGGGTTTGTAGAGCTTATTCACAAATGAGGATGTACTTGGGACATTTGAT 1860
 QY 1861 ACCACCCAGAUUAAUAAACUUCUCCUUGACCCGCCCCACCAAAAGAGUAGAUG 1920
 DB 1861 ACCACCCAGATTAATAAACTTCTCCCTTTCAGCCGCCCCACCAAAAGAGATG 1920
 QY 1921 CAGUUCUUCUACUGACUGUAGUAGUGAGGAGAACAGAAUAGAGAAUACUUGAAGGCGC 1980
 DB 1921 CAGTTCTCTTCAATGACTGTGAATGTAGGGGATCAGAAATGAGAAATCTTGTAAAGGCGC 1980
 QY 1981 AAUUCUCCUUAUUCACUACUACAGAGACCAACUAAAGAGACUAAUUAUUCUGGAAAGAU 2040
 DB 1981 AATTTCTCTGATTCACACTACACACAGACCACTAAGAGACTTAACTTCTCGAAAGAT 2040
 QY 2041 GCUGGACAUUUAACUGAAGACCCAGUAGAAAGCAUUCUGAGUGAGUCCGUGUUCUG 2100
 DB 2041 GCTGGCACTTTAACTGAAGACCCAGATGAAGGACATCTGGAAGTGCCTGCTTCTG 2100
 QY 2101 AGAGAGUCCUACUUCUGGCGAAAGAGAUAGAGAUUGGACCAAGAUUACCAUACAU 2160
 DB 2101 AGAGAGATTCCTCATCTTGGCGAAAGAGATGAGATGACACAGATTTAACATCAAT 2160
 QY 2161 GAACUGAGUAAACUUGGAGAAAGAGAAAGGCUAAUUGUAAUUGGCGAAAGAGACUG 2220
 DB 2161 GAACUGAGUAAACUUGGAGAAAGAGAAAGGCUAAUUGUAAUUGGCGAAAGAGACUG 2220
 QY 2221 GUGUGUUAUUGAAGCAAAACCGAACUCUAGCAUACUAGACAGCCAGACGACCC 2280
 DB 2221 GTGTTGTAATGAAACGAAACCGGACTTAGCATTTACTGACAGCCAGACAGGAGCC 2280
 QY 2281 AAAAGAGUUGGAGUGCCAUCAUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUA 2340
 DB 2281 AAAAGAGUUGGAGUGCCAUCAUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUA 2340
 QY 2341 U 2341
 DB 2341 T 2341
 RESULT 2
 ABA93934 ID ABA93934 standard; DNA; 2341 BP.
 AC ABA93934:
 XX 07-MAY-2002 (first entry)
 XX Influenza A/Udorn/72 (H3N2) Strain PB2 encoding DNA SEQ ID NO.1.
 DE Influenza A/Udorn/72 (H3N2) Strain PB2 encoding DNA SEQ ID NO.1.
 XX Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
 KW Influenza A virus; genome; gene; ds.
 OS Influenzavirus A.
 OS
 XX
 FH Key Location/Qualifiers

FT CDS 28..2307
 FT /*tag= a
 FT /product= "PB2 protein"
 XX
 PN MO200200884-A2.
 XX
 PD 03-JUN-2002.
 XX
 XX 21-JUN-2001; 2001WO-US19826.
 PF
 PR 23-JUN-2000; 2000US-213650P.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 XX Galarza JM, Latham TE;
 PI
 DR WPI; 2002-139923/18.
 DR P-PSDB; ABB05764.
 XX
 PT Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
 PT polypeptide, useful in diagnosis and for generating new influenza A
 PT variant strains
 XX
 PS Claim 1; Page 44-47; 103pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (1) having
 CC the complete sequence of the Influenza A/Udorn/72 (H3N2) strain in
 CC positive strand, antigenomic message sense. ABA93934 to ABA93944 encode
 CC the Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to
 CC ABB05774 from the present invention. (1) is useful for designing
 CC polymerase chain reaction (PCR) primers for use in a PCR assay to detect
 CC the presence of the corresponding virus segment in a sample or for
 CC designing and selecting peptides for use in an enzyme linked
 CC immunosorbent assay to detect the presence of the corresponding protein
 CC produced by that segment in a sample, hence is useful in diagnosis and
 CC may be modified by mutation to generate new influenza A variant strains.
 CC ABA93945 to ABA94039 represent Influenza A/Udorn/72 (H3N2) strain
 CC sequencing primers, which are used in an example from the present
 CC invention.
 XX
 SQ Sequence 2341 BP; 794 A; 419 C; 587 G; 541 T; 0 other;
 Query Match 92.8%; Score 2173; DB 24; Length 2341;
 Best Local Similarity 73.3%; Pred. No. 0;
 Matches 1715; Conservative 521; Mismatches 105; Indels 0; Gaps 0;
 QY 1 AGCGAAGCAGGUCUUAUUAUUAUUGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 60
 DB 1 AGCGAAGCAGGUCUUAUUAUUAUUAUUGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 60
 QY 61 UCGCAGUCUGCAGUCUGGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 120
 DB 61 UCGCAGUCUGCAGUCUGGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 120
 QY 61 TCGAGTCTCGCAGCTCGGAGATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 120
 DB 61 TCGAGTCTCGCAGCTCGGAGATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 120
 QY 121 AAGAGUACAUACAGGAGGAG 180
 DB 121 AAGAGUACAUACAGGAGGAG 180
 QY 121 AAGAGUACAUACAGGAGGAG 180
 DB 121 AAGAGUACAUACAGGAGGAG 180
 QY 181 GCAUUGAAUUAUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 240
 DB 181 GCAUUGAAUUAUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 240
 QY 241 GAGCAAGGCAAAACUUAUUGAGUUAUUAUUGAGUUAUUAUUGAGUUAUUAUUGAGUUAU 300
 DB 241 GAGCAAGGCAAAACUUAUUGAGUUAUUAUUGAGUUAUUAUUGAGUUAUUAUUGAGUUAU 300
 QY 301 UCAUCCUGCUGUAGUAGUGUAGUUAUUAUUGAGUUAUUAUUGAGUUAUUAUUGAGUUAU 360
 DB 301 UCAUCCUGCUGUAGUAGUGUAGUUAUUAUUGAGUUAUUAUUGAGUUAUUAUUGAGUUAU 360
 QY 301 TCACCTTTGGCGGTGATGAGTGAATGAATGAATGAATGAATGAATGAATGAATGAAT 360
 DB 301 TCACCTTTGGCGGTGATGAGTGAATGAATGAATGAATGAATGAATGAATGAATGAAT 360
 QY 361 CCAAAAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 420
 DB 361 CCAAAAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 420

Oy	421	CCUGUCUUVUUGAAACCAAGUCUAAAUAAGCCCGAAGUUGACUAUAAUUCUGUCUAC	480
Db	421	CTGTGCAATTTTAGAAACCAAGTCAAAATACGCCCAAGAGTTGACATTAACCTGTGCAT	480
Oy	481	GCAAGACUUCAGUCCGAAGGACACAGAUUGUAUACUAGAAAGUUGUUCUUAACGA	540
Db	481	GCAGACCTCAGTGCCAGAGGACAAAGATGTATCATGAAAGTTGTTTTCCCAATGAA	540
Oy	541	GUGGGGGGCCAGAUACUACGUCGGAUUCGCAUUAACAAUAAACCAAGAAAAAGAA	600
Db	541	GTGGGGGGCAGAGATCTAAACGTGGAATCACAATTAACAAATTAACAAAGAAAAAGAA	600
Oy	601	GAAACUCCAGAUUGCAAAAUUUUCACCUUUGAGUGUGGUAUAGUUVUUGAGAGAAACU	660
Db	601	GAACTCCAGATTCGCAAAATTTCTCTTGAATGTTGCATACATGTTTAAAGAGAACTT	660
Oy	661	GUCCGAAAAACGAGAUUUCUCCAGUUGUCUGUGGAAACAGCAGUGUUGACAUUGAAG	720
Db	661	GTCCGAAAAACGAGATTTCTCCCAATGCTGGTGGAAACAGACAGTGTATCATTTGAAGTG	720
Oy	721	UUGCAGCTUUGACUAGAAAGAAUAGUCUGGGAACAGUUGUACUCCACGUGUGGAAAGU	780
Db	721	TTACACTTGAACCTCAAGAAACGTGTGGGAACGATGTACACTCCAGGTGGGAAAGTGAAG	780
Oy	781	AUUGUAGUUGUUGAUCAAAAGUCUAAUUUUUUGCAGCCAGAGCAUUGGUAAGAAAGCAG	840
Db	781	AATGACGATGTGTACCAAAAGCCTTAATTTATGACGACGAGAACATGTAGAAAGACACCA	840
Oy	841	GUUUCAGCAGAUCCACUAGCAUUCUUUAUUGAGAUUGCCACAGCACAACAGUUGGCGGG	900
Db	841	GTATCAGCAGATCCACTAGCATCTTTATTTGAGATGTGCAACAGCACACTGATTTGGCGGG	900
Oy	901	ACAAGGAGUGUGACAUUCUUAUGGACGAACCCACAGAAAGCAACUCUGGAAAUUAGC	960
Db	901	ACAAGAGATGTGTGGAATCTTAGGCAGAACCCGACGAAAGAACAAAGCTGTGATTTATGAC	960
Oy	961	AAGGCUAGCAUUGGAGCUGAGAGUACGUCUACUCCUACGUUGGCGGGUUCACUUUAAG	1020
Db	961	AAGGCTGCAATGAGACTAGAGATCAGCTCATCTCTTCAGTTTGGTGGGTTCACATTTAAG	1020
Oy	1021	AGAACCAAGCGGUAUCAGUCAGUCAGAGAGAGAGAAAGUGUCUACCGGCAUUCUCAAACA	1080
Db	1021	AGAACCAAGCGGGTCATCAATCAATCAAAAGAGAGAAAGTGTCTTACCGGCAATCTCCAACA	1080
Oy	1081	UUGAAAAUAAAGGUGUCUAGCAGGGAUACGAGAGUUCACAUUGGUGUGGAAAAAGGCAACA	1140
Db	1081	TTGAAAAATAAAGGCTCATGAGGGGTACGAGGGTTCACAATGTGTGGGAAAAAGGCAACA	1140
Oy	1141	GCUAUACUAGAAAAAGCAACCGAGAUUUGUUGCAGUUAUGUGAGUGGAAAGACAGAA	1200
Db	1141	GCTATATCTAGAAAAAGCAACCGAGATTTGTTCAAGCTTATATGTAGATGGAAGGAGCAAG	1200
Oy	1201	CAGUCGAGAGCUGAAGCAAUAAUUGUGGCAUGUGUAUUUUCACAAAGAUUUGUAUUGAUA	1260
Db	1201	CAGTCAATATCGGAAGCGCAATATTGTAGCAGATGCTTTTCAACAAGAGATTGCAATGATA	1260
Oy	1261	AAAGCAGUAGAGUGUAGUUCGUAUUUCGUUUAUAGGGCAAAUACAGCAUUGAUAUCCCAUG	1320
Db	1261	AAAGCAGTTAGAGTGACCTGCAATTTCTGTTAAACAGGGCAAAUACACGGTGTGAATCCCAATG	1320
Oy	1321	CAUCAAACUUUUAAGCAUUUUCAGAAAGAGUUGGAAAGUCUUUCAAUUUUGGGGAUUU	1380
Db	1321	CATCAACTTTTAAAGCATTTTACAGAAAGATGCGAAAGTCTTTTTCAGATTTGGGGAAATT	1380
Oy	1381	GAACCAUUAUCAGCAUUGAGUGGAAUAGAUUGGGGUAUUAACGACAGUACUCCAAAGACA	1440
Db	1381	GAACATATTCGACAAATGTGATGGGAATGCTTGAAGTATTAACGACATGATCTCAAGACACA	1440
Oy	1441	GAGAUUCUACUAGAGAGGGGUAAAGAGUCACGCAAAAUUGGGCGUAUGAUAUUCUACGCGG	1500
Db	1441	GAGATGTCAATGACAGGAATTAAGAGTCAAGCAAAAUUGGGGCGTGAATATCTCCAGACACA	1500

QY	1501	GAGGAGUUAUGUGAGUCAGUACCCGGUUNUUGAUUUCUGAGCCAAACAGAGAAAGUA	1560
Db	1501	GAGGAGGAGTGGTTAGCATTTGATCGGTTTTTGAAGATTGAGAGCCAAAGTGGAAATGTA	1560
QY	1561	CUKCUAUCUCUCUGAGAGGUCAGUAGAAACAAGGGAAACAGAGAAACUGACAUUACUUC	1620
Db	1561	TTACTATCTCTCGTAGAGAGGTCAAGTAAACAAGGGGACAGAGAGACTGACAAATTAATTAC	1620
QY	1621	UCAUUGUUAUUGUGGGAGAUUUAUAGGCCUGAGUCAGUGUUGUGUCAAUACCUUACAG	1680
Db	1621	TCATCGTCAATGAATGTGGAGATTTAAATGGCCCTGAGTCAAGTGTGTCAATACCTATCAA	1680
QY	1681	UGGAGUVCUUCAGAAACUGGGGAAACUGUUAUUAUUCAGUGUCUCGAAUUCUACAUUCGUA	1740
Db	1681	TGGATTCATCGAGAAACCTGGGAAACGTTTAAATTCATTAAGTCTCAGAAATCTCAAAATGTTG	1740
QY	1741	UACAAUAAAAUUGAUAUUGAGCCCAUUCAGUCUUAAGUUCUUAAGGCCAUUUGAGGCCAA	1800
Db	1741	TACAAACAAATAGAAATTTGAGCCATTCAAGTCTTAATTCTTAAGGCCATTAGAGGCCAA	1800
QY	1801	UACAGUGGUGUUGUUGAGACUCUAUUCCAAACAAUAGAGGAUGUAUUUGGGACAUUUGAU	1860
Db	1801	TACAGTGGATTTGTCAAGAACTCTATTTCCAAACAAATGAGGAGATGACTTGGGACATTGGAT	1860
QY	1861	ACCACCCCAAGUAAUAAUAAUUCUUCUCCUUGBCAGCCGCCCCCAACCAAGCAAAGUAGAUG	1920
Db	1861	ACCACCCCAAGATMAATMAAGCTTCTCCCTTTGGCACGCCCCCAACCAAGCAAAGTAAATG	1920
QY	1921	CAGUUCUCUCUACUGACUCUGUAUGUUGAGGGGAAUCAGAAUAGAAUUAUUCUUGUAAAGGCC	1980
Db	1921	CAGTTCTCTTATTTGACTGTGAATGTAGGGGGATCAGGGATGAAGATCTTGTAAAGGGC	1980
QY	1981	AUUCUCCCUAAUUAUUCACUAACAACAAGACCAUAAGAUAUAUUAUUCUCGAAAGAU	2040
Db	1981	AATTCTCTCTGATTTCAACTACAAACAAGCCACTMAAAGACTPAACAATTTCTGGAAAGAT	2040
QY	2041	GCUGGCACUUAUCUGAAGACCAGAGUAGAGGCACAUUCUGAGUGAGUCCCGUGUCUG	2100
Db	2041	GCTGGCACTTTAATTGAAGACCACAGATGAAAGCACATCCGGAGTGGAGTCCGCTGTTTG	2100
QY	2101	AGAGGAGUUCUCUAUUCUGGGCAAGAAAGAUUAGAGAUUUGGACAGCAUUAUAGCAU	2160
Db	2101	AGAGGATTTTTCATTTCTAGATTAAGAAAGATTAAGAAATACGACCAAGCATTTAAGATCAAT	2160
QY	2161	GAUCUCUGAUAACUUGGCGAAAGAGAAAGGCUUAUGUAUUAUUGGCGAAAGAGACGUG	2220
Db	2161	GAACTGAATACCTTTGCAAAAGAGAAAGGCTAATGTGCTAATTTGGGCAAGAGAGACGTG	2220
QY	2221	GUGUUGUUAUUGAAGCAAGAAACGSAACUCUAGCAUUAUCUGACAGCCAGACAGCGAC	2280
Db	2221	GTTGTTGGTAATGAAGAAACGAAACGGGAGCTCTAGCACTACTTACTGTGACAGCAAGCGACC	2280
QY	2281	AAAAAGAUUCCGAGUAGGCCAUUAUUAUUGUUGAUAUAGUUAUAAACGACCUUGUUUCAC	2340
Db	2281	AAAAAGAAATTCGATGGCCATCAATTAATGTTGAATAGTTTAAACGACCTTGTTCAC	2340
QY	2341	U 2341	
Db	2341	T 2341	
RESULT 3			
AAK82192			
ID	AAK82192 standard; DNA; 2341 BP.		
XX	AAK82192;		
XX	18-AUG-1999 (first entry)		
XX	Influenza virus PB2 protein gene sequence.		
XX	Cold-adapted influenza virus; passage culture; PB2 protein; PB1 protein;		
KW	PA protein; NP protein; M protein; NS protein; temperature sensitivity;		

KW vaccine; flu; influenza; ss.
 XX Influenza virus.
 XX MO9928445-A1.
 XX 10-JUN-1999.
 XX 30-NOV-1998; 98WO-KR00384.
 XX 29-NOV-1997; 97KR-0064854.
 XX (CHEI-) CHEIL JEDANG CORP.
 XX Cheoun KH, Kim HG, Kim J, Kim SJ, Lee KH, Seong BL,
 XX Youn JW;
 XX WPI; 1999-385377/32.
 XX Cold-adapted influenza viruses useful for the production of
 XX protective vaccines against flu
 XX
 XX Claim 4; Page 50-51; 62pp; English.
 XX The invention relates to cold-adapted influenza viruses prepared by
 XX passage culture of A/X-31, B/Yamagata/16/88 or B/Lee/40 viruses at low
 XX temperatures. A cDNA gene of cold-adapted influenza virus H7CA-A101 can
 XX be selected from a group consisting of PB2 protein gene, PB1 protein
 XX gene, PA protein gene, NP protein gene, M protein gene and NS protein
 XX gene (AA82197-X82197). The method is useful for the production of cold-
 XX adapted influenza virus that exhibit temperature sensitivity and can be
 XX actively grown in fertilized eggs. The virus is useful for vaccines for
 XX protection against flu. Live vaccines containing cold-adapted viruses
 XX have several advantages over killed vaccines. It can prevent reduction
 XX of immunogenicity, which may occur in the killed vaccine where antigenic
 XX proteins would be denatured at its inactivation. It can also avoid
 XX hypersensitivity due to the prolonged administration of heterologous
 XX proteins. It promotes the immunity by inducing IgA and it can be
 XX administered into a spray formulation via nasal cavity and thus its
 XX application is convenient for children. It is able to inhibit the
 XX growth of the wild-type virus and thus its therapeutic effect can be
 XX expected. The present sequence represents the influenza virus PB2
 XX protein gene.
 XX
 XX Sequence 2341 BP; 785 A; 423 C; 597 G; 536 T; 0 other;
 XX
 XX Query Match 90.2%; Score 2110.6; DB 20; Length 2341;
 XX Test Local Similarity 72.2%; Pred. No. 0;
 XX tches 1690; Conservative 507; Mismatches 144; Indels 0; Gaps 0;

QY 361 CCAAAAACUACAAACUUAUUUGAAGAAAGUCAAAGUUAACUAGAACUUTUGGC 420
 DB CCAAAAATCTACAAATCTTATTTGAAAGAGTCCAAAAGGCTAAAGATGAAACCTTTGGC 420
 QY 421 CUGUCCAUUUUAGAAAACCAAGUUAUUGCCGAAGAGUGGCAUUAUUCUGUGCAU 480
 DB CUGUCCAUUUUAGAAAACCAAGUUAUUGCCGAAGAGUGGCAUUAUUCUGUGCAU 480
 QY 421 CUGUCCAUUUUAGAAAACCAAGUUAUUGCCGAAGAGUGGCAUUAUUCUGUGCAU 480
 DB CUGUCCAUUUUAGAAAACCAAGUUAUUGCCGAAGAGUGGCAUUAUUCUGUGCAU 480
 QY 481 GCAGACCUAGUGGCCAAGAGAGGCAAGAGUUAUUGAAGUUAUUGCCUUAACGAA 540
 DB GCAGATCTCAGTGCAGAGAGGCAAGAGATGATATCATGAAAGTGTTCCTTAAGAA 540
 QY 541 GUGGGGCGCAGAGUUAUUAAGUGGAAUUGCCAAUUAUUAACAAAGAGAAAGAA 600
 DB GTGGAGCCAGAGATCTACATCGAATCCCACTAACATGATTAACAAAGAGAAAGAA 600
 QY 601 GAACUCCAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 660
 DB GAACUCCAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 660
 QY 601 GAACUCCAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 660
 DB GAACUCCAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 660
 QY 661 GUCCGAAAACGAGAUUUUCCAGUGUGUGGAAACAGAGUGUGUACUUAAGAGUG 720
 DB GUCCGAAAACGAGAUUUUCCAGUGUGUGGAAACAGAGUGUGUACUUAAGAGUG 720
 QY 661 GUCCGAAAACGAGAUUUUCCAGUGUGUGGAAACAGAGUGUGUACUUAAGAGUG 720
 DB GUCCGAAAACGAGAUUUUCCAGUGUGUGGAAACAGAGUGUGUACUUAAGAGUG 720
 QY 721 UUGCAUUGACUUAAG 780
 DB UUGCAUUGACUUAAG 780
 QY 721 UUGCAUUGACUUAAG 780
 DB UUGCAUUGACUUAAG 780
 QY 781 AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840
 DB AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840
 QY 781 AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840
 DB AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840
 QY 841 GUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 900
 DB GUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 900
 QY 841 GUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 900
 DB GUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 900
 QY 901 ACAAGAGUGUGUACAUUUUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 DB ACAAGAGUGUGUACAUUUUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 QY 901 ACAAGAGUGUGUACAUUUUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 DB ACAAGAGUGUGUACAUUUUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 QY 961 AAGGUGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1020
 DB AAGGUGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1020
 QY 961 AAGGUGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1020
 DB AAGGUGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1020
 QY 1021 AGAACAAGGAGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1080
 DB AGAACAAGGAGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1080
 QY 1021 AGAACAAGGAGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1080
 DB AGAACAAGGAGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1080
 QY 1081 UUGAAG 1140
 DB UUGAAG 1140
 QY 1081 UUGAAG 1140
 DB UUGAAG 1140
 QY 1141 GCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1200
 DB GCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1200
 QY 1141 GCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1200
 DB GCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1200
 QY 1201 CAGUGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1260
 DB CAGUGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1260
 QY 1201 CAGUGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1260
 DB CAGUGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1260
 QY 1261 AAAGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1320
 DB AAAGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1320
 QY 1261 AAAGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1320
 DB AAAGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1320
 QY 1321 CAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1380
 DB CAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1380
 QY 1321 CAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1380
 DB CAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1380
 QY 1381 GAACAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1440
 DB GAACAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1440

[illegible]

DE	Mutant PB2 protein, ALA6, coding sequence.
XX	
KW	Influenza virus, PB2 protein; charged cluster; master donor virus;
KW	Influenza A virus A/LN/2/87; ALA1; ALA2; ALA3; ALA4; ALA5; ALA6;
KW	ALA7; ALA8; attenuation; viral phenotype; temperature sensitivity;
KW	vaccine; influenza virus A/Memphis/8/88; ss.
XX	
OS	Influenza virus.
OS	Synthetic.
XX	
FH	Key
FT	Location/Qualifiers
FT	28..2307
FT	/*tag= a
FT	/product= ALA6
XX	
FN	W09639179-AL.
XX	
PD	12-DEC-1996.
XX	
PE	03-JUN-1996; 96WO-US08441.
XX	
PR	05-JUN-1995; 95US-0462388.
XX	
PA	(AVIR-) AVIRON.
XX	
PI	Coelingh KL, Parkin NT;
DR	WPI; 1997-042859/04.
DR	P-PSDB; AAM07710.
XX	
PT	Recombinant influenza virus with mutation(s) in charged cluster
PT	regions - esp. temperature-sensitive mutation(s), has attenuated
PT	phenotype suitable in vaccines for preventing influenza
XX	
PS	Claim 7; Page -; 39pp; English.
XX	
CC	The sequences given in T75683-90 encode modified influenza virus PB2
CC	proteins, ALA1-ALA8. The modified proteins are generated by replacing
CC	certain Arg, Lys and Asp residues in one of 8 charged clusters
CC	identified in influenza A virus A/LN/2/87 PB2 protein, with Ala
CC	residues. Specifically, the mutations are as follows: ALA1 (residues
CC	2-6) ERIKE -> EAIAE, ALA2 (residues 120-124) DKVER -> DAVEA, ALA3
CC	(residues 140-144) KIRRR -> KIAAA, ALA4 (residues 187-192) KEKKE ->
CC	KEAEE, ALA5 (residues 339-343) KREEE -> AAEEE, ALA6 (residues 677-681)
CC	EDPDE -> EAPPA, ALA7 (residues 699-703) KEDRR -> KEDAA and ALA8
CC	(residues 736-740) KRKRD -> ARKRD. Recombinant influenza viruses which
CC	contain these mutations produce attenuated viral phenotypes, useful as
CC	master donor viruses in the preparation of immunogenic compositions,
CC	e.g. vaccines, for preventing influenza, or a disease associated with
CC	influenza infection. Modification of charged cluster residues result
CC	in consistent and predictable exhibition of temperature sensitivity.
CC	These sequences are not given in the specification and are based on the
CC	influenza virus A/Memphis/8/88 given in Genbank M73517.
XX	
XX	
Sequence	2341 BP; 802 A; 428 C; 575 G; 536 T; 0 other;
Query Match	89.5%; Score 2094.6; DB 18; Length 2341;
Best Local Similarity	71.7%; Pred. No. 0;
Matches 1678;	Conservative 509; Mismatches 154; Indels 0; Gaps 0
DB	
1	ACCGAAGCAGGUCUUAUUUUGCAUUUUGGAAAGAAUAAAGACUACGGAUUCUGAUC 60
1	ACCAAAAGAGGTCAATTAATTATTCAGTATGGAAAGATTAAGAACTACGGAACCTGATG 60
QY	UCCGAGUCUCGCGACUCGCGAGAUACAAACAAACACACGUGGACCAUUGGCCAUUAUU 120
61	UCCGAGUCUCGCGACUCGCGAGAUACAAACAAACACACGUGGACCAUUGGCCAUUAUU 120
DB	TGCGAGTCTCGGAGCTCGCGAGTACTTAACAAAACACAGCTGACCATATGCGCATTAATT 120
QY	AAGAAGUACACAUCAACGAGGACGAGAAAAGAAACCCGUCACUUGAUGAAAUAGUGAUG 180
121	AAGAAGUACACAUCAACGAGGACGAGAAAAGAAACCCGUCACUUGAUGAAAUAGUGAUG 180
DB	AAGAAGTACACATCTCAGGAGAGAGAGAAAAGAAACCCGTCCTTAGAGATGAATAATGATGATG 180
181	GCAUUGAAUUAUUNCCGATUUNACGCCGACAAAGAGAUAAAGAAUUAUUCUGAGAGAAU 240

DB 181 GCATGAAATATCCAAATCACTGCTGACAAAAAGATTAACAAATATGTTCCGAGAGAAAT 240

QY 241 GAGCAAGGGCAAACTCUCUUGAGUAAAAUAGUGAUGCCGAGUCGAGUCGUGAGUGUA 300

DB 241 GAAACAAGAGAAATCTATGGAATTAATGATGATCTGGGTCAAGATCAAGATATGTA 300

QY 301 UCAACCCUGGCGUGAUCAGUGUGGAAUAGAUAUGAACAAUGACAAGUAACGUAUCUUAU 360

DB 301 TCACCCCTTGGCAGATGACATGATGGAATATGAATATGACCAATGTACAAATACGGTTCACTAT 360

QY 361 CCAAAAATUCUACAAACUUAUUTUGAAGAAAGUCGAAAGUUAAAAUAGAACCTTUGGC 420

DB 361 CAAAAGTCTACAAAGACTTATTTTGGCAAAAGTGAAAGTTTAAACATGTAAACCTTTGGC 420

QY 421 CCUGUCUUAUUUGAAAAACAAAGUCAAUUUACGGCAAGAGUUGACUAAAAUUCUGUCAU 480

DB 421 CCGTGTCACTTTTGAATTCAGATCTCAAAATATGCGCAAGATATGACATTAACCTTGATCAT 480

QY 481 GCAGACCTUACGUGCCCAAGAGGACACAGAUUGUAUACAUGAAGUUGUUTUCCUACGA 540

DB 481 GCAGACCTAGTCCCAAGAGGACACAGATGTATATATGGAAGTTGTTTCCCAATGAA 540

QY 541 GUGGGGGCCACAGAUACUAAACGUCGGAUUGCCAUAUAAACAAAGAAAAAGAA 600

DB 541 GTGGAGGCCAGGATACTTAACATGAGATCAAAATTAAACAATTAACAAAGGAAAAAGAA 600

QY 601 GAAUCUCAGAGUUGCAAAAUUUCACCUUGUUGUGUGUAUUGUUGAGAGAGAAACU 660

DB 601 GAACTCCGAGATTTGCCAAATTTTCTCTTTGATGTTGATCAATGTTAGAGAGAACTT 660

QY 661 GUCCGAAAAACGAGAUUUCUCCAGUGUCUGUGUGAAACAAGUGUGUAUUGAAGUG 720

DB 661 GTCCGAAAAACGAGATTTCTCCAGTTGCTGTGGAAACAAGCAGTATATACATTAAGTT 720

QY 721 UUGCACTUAGCUCUAAAGAACUUCUGGGAACAGAUUGUACAUCUCAGUGGAGAGUGAG 780

DB 721 TTACATTTTACCTCAAGAAACGTGTTGGGAAACAAATGTACCTCAAGTGGAGAAAGTGAAG 780

QY 781 AAUGATGAGUGAUCUAAAGUCUAAAGUCUAAUUGUUGACCGACGAGGCUUAUGAAGAGACGA 840

DB 781 AATGACGATGTTGACCAAAAGCCTTAATTTTGCACCGAGAACCTATGTGAAGAGCGCA 840

QY 841 GUUACGACGAGUCCACUACGACUUCUUAUUGAGAUUGGCGACACAGACAACAAGUUGCGGG 900

DB 841 GATACGACGATCCACTAGCATCTTTATTAAGAGATGTGCCACAGCACACAAATTTGGCGGG 900

QY 901 ACAAGAGUGGUGACAUUCUUAUGGCAAAACCAACGAAAGACGACAGUCUGGAAUAUUC 960

DB 901 ACAAGAGATGTGGACATTTCTTAGGCGAAACCCGACGAAAGAACAGCTGTGATATATGC 960

QY 961 AAGGCGUACAAUUGGACUGAGGACUACUCUACUUCUUAUGGUGCGGUGUCUUAUAG 1020

DB 961 AAGGCGCAATGGGACTGAGAAATCACCTCATCTTAGCTTGGTGGTTCACATTTTAA 1020

QY 1021 AGAACAGCGGAGUACUACGACUCAAAGAGAGAGAAAGUUCUUAUCGCGCAUUCUCAAACA 1080

DB 1021 AGAACAGCGGGTCCCTCATTCAAAAAGAGAGAAAGATGCTTACAGGCAATCTCCAAACA 1080

QY 1081 UUGAAAAUAAAGGUGUGCUGAGGAGUACGAGAGAGUUCACAUAUGUGUGGAAAAAGGCACACA 1140

DB 1081 TTGAAAAATTAAGATGCATAGGGGGTACGAGAGATTACAAATGGTGGGAAAAAGGCGACACA 1140

QY 1141 GCUAAUUCUAGAAAAAGCAACGAGAGAUUUGUACUUCUUAUUGUUGUGGAAAGACACGA 1200

DB 1141 GCTATATCTAGAAAAAGCAACGAGAGATTTGTTCACCTCATATGTGTGTAAGAGGACGGA 1200

QY 1201 CAGUCGAGUAGCUGAGCAUUAUUTUGUGCCCAUGGCUUAUUTUACAAGAAAGAUUGUAUGUA 1260

DB 1201 CAGTCAATAGCCGAAACCAATATATCGTAGCCATGTGTTCACAAAGAGATTTGCATGATA 1260

QY 1261 AAAAGCAGUAGAGUGAUCUGAAUUTUGCUUAUUGGGCAAAUUCGAGUUAUCCCAUG 1320

Db	1261	AAAGCAGTTAGAGTGACCTGTAATTTGCTTAACAGGGGCAAAATCAGCGGTGAATCCCATG	1320
QY	1321	CAUCAAACUUYUUAAGAUAUUTUCAGAGAAGUGCGAAAGUGUCUUYUCAAAUUTUGGGGAUUT	1380
Db	1321	CATCAGCTTTTAAGGCACTTTTCAGAAAAGATGCGAAAGTCTTTTCAGAAATTTGGGGAATT	1380
QY	1381	GAACUAUUCGACAAUUGUAGUGGGAAUGAUUGGGGUUAUCCAGACUAUGACUCCAAAGCA	1440
Db	1381	GAACATATTCGACACAGTGATGATGGGAAATGGTTGGAAGTAATTACAGATATTACTCCAAAGCA	1440
QY	1441	GAGAUATGUAUAGAGGAGGUAAGAGUCAGCAAAAUUGGCGUAAGAUUAUACUCCAGCGCG	1500
Db	1441	GAGATGTCAMATGAGAGGAATTAAGATGAGCAAAATTTGGCGTGGATGAAATATCTCCAGCA	1500
QY	1501	GAGAGAGUAGUGUGUAGUAUGACCGGUTUUYUAGAGUUYUGAGACCAACGAGAGAAUUGUA	1560
Db	1501	GAGAGGGTGGTGGTTAGCATGATTCGGTTTTCAGAGATTCCAGACCAACGTGGGAAATGA	1560
QY	1561	CUACUAUCCUCUGAGAGAGUACAGUAAACACAGGGAAACAGAGAAACUGACAAUUAUUAUAC	1620
Db	1561	TTACTATCTCCTGAGAGAGTGTCAGTGAACACAGGGAAACAGAGACATGACAAATTAATTAC	1620
QY	1621	UCAUUGUUAUAGUUGUGGAGAUUAUUGGCCUCUAGUACUGUUGUUCUAUACCUAUACAG	1680
Db	1621	TCATCTGTCAMATGAATGTGGGAATTAACGCGCCTTAGTCGAGTGGTTCMAATATCTATCA	1680
QY	1681	UGGAUACACAGAAACUGGGAAACUGUUAUAUUYUAGUGUUCUGAAUUCUACAAUUGUA	1740
Db	1681	TGGATCATCAGAAATTTGGGAAACTGTTAAATTCMAATGATTCAGAAATCTCGCAATGTTG	1740
QY	1741	UACAAUAAAUGGAUUTUGAGCCAUUUCAGUCUUYUAGUCUUAAGCCAUUUAAGGCCAA	1800
Db	1741	TACAACAAAAATGGAAATTTGAACCAATTCAGTCTTAAGTTCTTAAGGCCATTAGAGGCCAA	1800
QY	1801	UACAGUGGUGUUGUUGAGACUUCUAUUCACAAAUAGAGGAUGUAUUTUGGGACAUUTUGAU	1860
Db	1801	TACATGTGATTTGTTCAGAACTCTATTCCAACMAATGAGATGTACTTGGGACATTTGAT	1860
QY	1861	ACCAACCCAGUAUAAAACUUCUUCUCCUUGCACCGCGCCCAACAAAGCAAGAAUGAAUG	1920
Db	1861	ACCAACCCAGATTAATAAGCTTCTCCTCTTTGACACCGCTCCACCAACAAAGCAAGCAGATG	1920
QY	1921	CAGUUCUCUCUACUAGCUCUGUAGUAGUGGAGUACAGAAUUGAGUAUACUUGUUAAGGGGC	1980
Db	1921	CAGTTCTCTCATTTGACGTGTGAATGTGAGGGGATCAAGGAAATGAATAATCTGTAAAGGGC	1980
QY	1981	AAUUCUCCUAUUAUUAACUAACAAAGACCAUUAAGACUAUACUUCUGGAAAGAGU	2040
Db	1981	AATTCCTCTGTATTTCAACTACAAACAAAGCCACTAAAGACTTACAAATTTCTCGAAAAAGAT	2040
QY	2041	GUUGGCAUUYUAUCUGAAGACCCGAGUAGAAAGGCAUUCUGAGUGUGAGUCCGUGUUG	2100
Db	2041	GCTGGCACTTTAATTGAAGACCCCAAGCTGCAAGCAATCCGAGTGGAGTCCGCTGCTTG	2100
QY	2101	AGAGAGUUCUCUAUUCUGGCGAAAGAGAUUAGAUUAGACCCAGACUUAUUAAGCAUUAU	2160
Db	2101	AGAGGATTTTCTCATTTCTAGATGAAGAAAGCAAGAGATACGAGACAGCATTAAGCATCAT	2160
QY	2161	GAACUAGUAUACCUUGCGAAAGAGAAAGGCUUAUGUAUUAUUGGCGAAAGAGACGUG	2220
Db	2161	GAACTGAGTAACTTTGCAAAAAGGGGAAAGGCTAATGTGCTAATTTGGGCAAGGAGAGTGT	2220
QY	2221	GUUUGUGUAUAGAAACGAAACGGAACUCUAGCAUUAUUAUUCUGACCCAGACGAGCACC	2280
Db	2221	GTTGTTGGTAATGAAGAAACGAAACGGGACTCTAGCATTAATGACAGCCAGACGCAACC	2280
QY	2281	AAAAGAUUUCGAGUGGCCAUCAUUAUUAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAU	2340
Db	2281	AAAAGAAATTTGGAGTGGGCATCAATTAATGTTGAATATGTTTAAAGAGACCTTGTTCATC	2340
QY	2341	U 2341	
Db	2341	T 2341	


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Qy 1141 GCUAUAUCUAGAAAAGCAACGAGAGUUGUACGUGUUGUGAGUGGAAAGACGAA 1200
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1141 GCTACTCTGAAAAAGACACAGAGATGTGTTCACTGATGATGATGAGAGACGAA 1200
Qy 1201 CAGUCGUAUACUGAAGCAUAUUGUGCCAUUGUUAUACAGAAAGAUUGUUAUA 1260
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1201 CAGTCATATACCGAGAAATATCGTAGCAATGTGTTTCAAGAAAGATTCAGATA 1260
Qy 1261 AAAGCGUUAAGGUGUUGUUAUUGUGUUAUAGGCGCAAUACGCGAUUAGUCCAU 1320
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1261 AAAGCGATTAGAGGTGCTGAAATTCGTTTACAGGCGCAAAATCGAGTTGAAATCCATG 1320
Qy 1321 CAUCAAUCUUUUAAGACAUUUUUAAGAGAGGAAAGUGCUUUUUAAGAAAUUGGGGGAUU 1380
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1321 CATCAGCTTTTAAAGCATTTTTCAGAAAGATGCGAAAGTGCTTTTTCAGAAATGGGGAATT 1380
Qy 1381 GAACAUUUCGACAUUGGAGUUGAGUUGUGGGUUAUUAACAGACAUUCUACAGACA 1440
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1381 GAACATATCGACAGTGTGATGAGATGTGTTGAGTATACAGATATGATCTCCAAACACA 1440
Qy 1441 GAGAGUCUAUAGAGGGGUAAGUUCAGCAAAAUUGGCGUAGUUAUUCUACGCGG 1500
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1441 GAGATGTCAATGAGAGGAATTAAGATCAGCAAAATGGCGTGATGAAATACCCAGACA 1500
Qy 1501 GAGAGUUGUGUGUAGCAUUGACCGGUUUUUGAGUUGUUGAGACCAAGAGAAAUUGA 1560
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1501 GAGAGGGTGTGTGTGACATTTGATGCGTTTAAAGAGTTTCAGAACCAAGTGTGAAATGTA 1560
Qy 1561 CUACUUAUCUCUGAGAGGUCAGUAGAAACAGAGGAAACAGAGAAACUGACAUUAUCU 1620
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1561 TTACTATCTCTGAGAGAGTCACTGAAACAGAGGAAACAGAGACTGCAATTAATTAC 1620
Qy 1621 UCAUUGCUAUGAUGUGGAGAUUAUUGCCUUGAGUCAGUGUGUCUAUAUCUACG 1680
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1621 TCATCTCATATGATGTGTGAGATTAACGCGCTGAGTCCGTTGTCATATCTATCAA 1680
Qy 1681 UGGAUCUAUGAGAAACUGGAAACUGUUAUAUUCAGUGUCUACAUUCUACUACG 1740
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1681 TGGATATCATGAATGAGAACTGTTAAATTCATTAATGCTTCAGAAATCTTCATATGTTG 1740
Qy 1741 UACAAUAAAUAGGAUUGAGCCAUUUCAGUCUUAUUGUUCUUAAGGCCAUUUGAGCC 1800
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1741 TACAAATAAATGGAATTTGACATTTCACTTTAGTTCTTAAGGCCATTTAGAGCCAA 1800
Qy 1801 UACAGUGGUGUUGUUGAGACUCUUAUUCACAAAUAGGAGUAGUACUUGGAGCAU 1860
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1801 TACAGTGAATTTGTGCAACTCTATTCACAAATAAGAGATGTACTTGAGCATTTGAT 1860
Qy 1861 ACCACCCAGAUUAUAAACUUCUCCUUGCAGCCGCCCAACAAAGCAAAAGUAGAU 1920
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1861 ACCACCCAGATATTAAGCTTTCCTTTTTCAGCGCTTCACAAAGCAAAAGCAGATG 1920
Qy 1921 CAGUUCUCUUCACUGACUGUUAUGAGGAGGAGUACGAUAGAUACUUGAGGGG 1980
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1921 CAGTTCCTCTCATGTGACTGTGAATGTGAGAGGATCAGGAGTGAATCTTGTAAAGG 1980
Qy 1981 AAUUCUCUUAUUAUUAACUACACAAAGACACUUAAGAGACUUAUUCUCGAAAGAU 2040
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1981 AATTCTCTGTATTCATTAACAAACAGACACCTAAAGACTTAATCTCGGAAAGAT 2040
Qy 2041 GUGGACAUUAACUGAAGACCCAGAUAGGACAUUCUGAGUGGAGUCCGUCUUCUG 2100
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2041 GCTGGACATTTAAATTGAAAGACCCAGATGAACACACTCCGAGTGTGAGCTCTCTTG 2100
Qy 2101 AGAGAUUUCUACUUCUGGCAAAAGAGUAGAGAUUAGGACCAUUAUUAUUAU 2160
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2101 AAGAGATTTCTCATTTCTAGTAAAGAGACAGAAAGTATGAGGACAGCATTAAGCAT 2160
Qy 2161 GAACUGAGUACCCUUGCGAAAGAGAAAGCGCUAUAUUGGCGCAAGAGACGUG 2220
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2161 GAACGTAGTAACCTTGCAAAAGGCGAAAGGCTTAATGTCTAATTGGGCAAGAGACG 2220
Qy 2221 GUGUUGUUAUUAAGAAACGAAACGGAACUCUAGCAUAUCUACAGCAGCAGCGAC 2280

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Db 2221 GTGTTGTAATGCGCAAAAAACGAGACTCTGACTTACTGATGACAGCCAGACGAC 2280
Qy 2281 AAAAGAUUCGAGUGGCAUUAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2340
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2281 AAAAGAAATTCGAGGCGCATATTAATGTTGAATAGTTTAAAAACGACCTGTTT 2340
Qy 2341 U 2341
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2341 T 2341

RESULT 6
AAT75686
ID AAT75686 standard; cDNA; 2341 BP.
XX
AC AAT75686;
XX
DT 11-SEP-1997 (first entry)
XX
DE Mutant PB2 protein, ALA4, coding sequence.
XX
KW Influenza virus; PB2 protein; charged cluster; master donor virus;
KW influenza A virus A/LA/2/87; ALA1; ALA2; ALA3; ALA4; ALA5; ALA6;
KW ALA7; ALA8; attenuation; viral phenotype; temperature sensitivity;
KW vaccine; influenza virus A/Memphis/8/88; ss.
XX
OS Influenza virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 28..2307
FT /tag= a
FT /product= ALA4
PM M09639179-A1.
PD 12-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US08441.
XX
PR 05-JUN-1995; 95US-0462386.
XX
PA (AVIR-) AVIRON.
PI Coelighh KL, Parkin NT;
XX
DR WPI: 1997-042859/04.
DR P-PSDB: AAM07708.
XX
PT Recombinant influenza virus with mutation(s) in charged cluster
PT regions - esp. temperature-sensitive mutation(s), has attenuated
PT phenotype suitable in vaccines for preventing influenza
XX
PS Claim 7; Page -: 39pp; English.
XX
CC The sequences given in T75683-90 encode modified influenza virus PB2
CC proteins, ALA1-ALA8. The modified proteins are generated by replacing
CC certain Arg, Lys and Asp residues in one of 8 charged clusters
CC identified in influenza A virus A/LA/2/87 PB2 protein, with Ala
CC residues. Specifically, the mutations are as follows: ALA1 (residues
CC 2-6) BRIKE -> EAIKAE, ALA2 (residues 120-124) DKVER -> DAVEA, ALA3
CC (residues 140-144) KIRRR -> KIIAA, ALA4 (residues 187-192) KEKKEE ->
CC KEAAEE, ALA5 (residues 339-343) KREBE -> AAEEF, ALA6 (residues 677-681)
CC EDDEE -> EAPPA, ALA7 (residues 699-703) KEDRR -> KEDAA and ALA8
CC (residues 736-740) KRKRD -> ARKRD. Recombinant influenza viruses which
CC contain these mutations produce attenuated viral phenotypes, useful as
CC master donor viruses in the preparation of immunogenic compositions,
CC e.g. vaccines, for preventing influenza, or a disease associated with
CC influenza infection. Modification of charged cluster residues results
CC in consistent and predictable exhibition of temperature sensitivity.
CC These sequences are not given in the specification and are based on the
CC influenza virus A/Memphis/8/88 given in Genbank M73517.

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XX Sequence 2341 BP; 800 A; 427 C; 577 G; 537 T; 0 other;
SQ
Query Match 89.3%; Score 2091.4; DB 18; Length 2341;
Best Local Similarity 71.6%; Pred. No. 0;
Matches 1676; Conservative 509; Mismatches 156; Indels 0; Gaps 0;

QY 1 AGCGAAGACAGGUCUAUUUAUUCUAUUGGAAAGAAUAAAAGAACUACCGAAUUCUGAUG 60
DB 1 AGCGAAGACAGGUCUAUUUAUUCUAUUGGAAAGAAUAAAAGAACUACCGAAUUCUGAUG 60
QY 61 UCCGAGUCUCGCAUUCGCGAGAUACUAAACAAACCAAGUGGACCUAUAUGGCCAUUAU 120
DB 61 UCCGAGUCUCGCAUUCGCGAGAUACUAAACAAACCAAGUGGACCUAUAUGGCCAUUAU 120
QY 121 AAGAAAGUACAUACAGGAGGACAGAAAGAAACCCGCAUCUAGGAGUAGAAUUGAUG 180
DB 121 AAGAAAGUACAUACAGGAGGACAGAAAGAAACCCGCAUCUAGGAGUAGAAUUGAUG 180
QY 181 GCAUAGAAAUUUCGAGUUAACGCCGACAAAGAGUAAACAGAAUUGAUUCCUGAGAGAAU 240
DB 181 GCAUAGAAAUUUCGAGUUAACGCCGACAAAGAGUAAACAGAAUUGAUUCCUGAGAGAAU 240
QY 241 GAGCAAGGCAAAUCUUAUGAGUAAAUAGUGUACCGGAGUUGCCUGUUGAUGUA 300
DB 241 GAGCAAGGCAAAUCUUAUGAGUAAAUAGUGUACCGGAGUUGCCUGUUGAUGUA 300
QY 301 UACACUCUGGUGUACUGUGGAGUAAUAGAACCAUAUGACAAUAGCAAGUACGUAUCUAU 360
DB 301 UACACUCUGGUGUACUGUGGAGUAAUAGAACCAUAUGACAAUAGCAAGUACGUAUCUAU 360
QY 361 CCAAAAAUCUACAAACUUAUUUUGAGAAAGUCGAAAGGUAUAAAACUGAACCCUUGGC 420
DB 361 CCAAAAAUCUACAAACUUAUUUUGAGAAAGUCGAAAGGUAUAAAACUGAACCCUUGGC 420
QY 421 CCUGUCCAUUUUAGAAACCAAGUCUAAAUACCCGAGAGUGUACAUAAUCCUGUACU 480
DB 421 CCUGUCCAUUUUAGAAACCAAGUCUAAAUACCCGAGAGUGUACAUAAUCCUGUACU 480
QY 481 GCACACUCUACUGGCAAGGAGGACAGGAGUUAUUGAUGAAAGUGUUAUCCUUAAG 540
DB 481 GCACACUCUACUGGCAAGGAGGACAGGAGUUAUUGAUGAAAGUGUUAUCCUUAAG 540
QY 541 GUGGAGGACAGAGUAUUAACGUCGGAUUCGCAUUAUACAAUAAACAAAGAGAAAAAGAA 600
DB 541 GUGGAGGACAGAGUAUUAACGUCGGAUUCGCAUUAUACAAUAAACAAAGAGAAAAAGAA 600
QY 601 GAACUUCAGAUUUGCAAAAUUUUACCUUUGAUUGUGUUGCUAUGUUAAGAGAGAACTU 660
DB 601 GAACUUCAGAUUUGCAAAAUUUUACCUUUGAUUGUGUUGCUAUGUUAAGAGAGAACTU 660
QY 661 GUCCGAAAAAGAGAUUUUUCGAGUUGCUGGAGAAACAGCAGUGUUAUUAUGAUG 720
DB 661 GUCCGAAAAAGAGAUUUUUCGAGUUGCUGGAGAAACAGCAGUGUUAUUAUGAUG 720
QY 721 UUGCAUCUUGCAAGAAACUUGCUGGAGAAAGAGUUAACUUCGUGGAGAGAG 780
DB 721 UUGCAUCUUGCAAGAAACUUGCUGGAGAAAGAGUUAACUUCGUGGAGAGAG 780
QY 781 AAUGAGUAGUUGAUCAAAUUCUUAUUAUUGCAGCAGAGCAUUGAGAGAGAGCA 840
DB 781 AAUGAGUAGUUGAUCAAAUUCUUAUUAUUGCAGCAGAGCAUUGAGAGAGAGCA 840
QY 841 GUAUCAGAGAUUCCAGUAGUUAUUUUGAGUAGUUGCCACAGACACAGAUUGGGGG 900
DB 841 GUAUCAGAGAUUCCAGUAGUUAUUUUGAGUAGUUGCCACAGACACAGAUUGGGGG 900
QY 901 ACAAGAGUGGAGACAUUCUUAUGAGAGAACCAACAGAGAGCAAGCUGUGAAAUUAGC 960
DB 901 ACAAGAGUGGAGACAUUCUUAUGAGAGAACCAACAGAGAGCAAGCUGUGAAAUUAGC 960
QY 961 AAGCUGGCAUUGGAGUAGAGUACGUCUUCUUCAGUUAUUUGGCGGUGUACAUUUAAG 1020
DB 961 AAGCUGGCAUUGGAGUAGAGUACGUCUUCUUCAGUUAUUUGGCGGUGUACAUUUAAG 1020

DB 961 AAGCUGGCAUUGGAGUAGAGUACGUCUUCUUCAGUUAUUUGGCGGUGUACAUUUAAG 1020
QY 1021 AAGAACAGCGGAGUUCUACUAGAGAGAGAGAGAGAGUUCUUAAGGCAUUCUUAACA 1080
DB 1021 AAGAACAGCGGAGUUCUACUAGAGAGAGAGAGAGAGUUCUUAAGGCAUUCUUAACA 1080
QY 1081 UUGAAAUUAAGUUCUAGAGAGUUAACAGAGUUAACAUUGUUGGAGAAAGGCAACA 1140
DB 1081 UUGAAAUUAAGUUCUAGAGAGUUAACAGAGUUAACAUUGUUGGAGAAAGGCAACA 1140
QY 1141 GCUUAUCACAGAAAGCAACAGAGAGUUAUCAGCUGAUUUGAGUGAGAGAGAGCA 1200
DB 1141 GCUUAUCACAGAAAGCAACAGAGAGUUAUCAGCUGAUUUGAGUGAGAGAGAGCA 1200
QY 1201 CAGUGCAUUGGAGAGCAUUAUUGUGGCCUUGGUUAUUUUCACAAAGAUUGUUA 1260
DB 1201 CAGUGCAUUGGAGAGCAUUAUUGUGGCCUUGGUUAUUUUCACAAAGAUUGUUA 1260
QY 1261 AAGGCAUUAAGGAGUACUUAUUUUGGCGAAAUUAGCGAUUCCAUUG 1320
DB 1261 AAGGCAUUAAGGAGUACUUAUUUUGGCGAAAUUAGCGAUUCCAUUG 1320
QY 1321 CAUCAAUCUUUAAGCAUUAUUCAGAGAGAGAGAGAGAGUUCUUAUUUGGGAUU 1380
DB 1321 CAUCAAUCUUUAAGCAUUAUUCAGAGAGAGAGAGAGAGUUCUUAUUUGGGAUU 1380
QY 1381 GAACAUUAUGCAUUGAGUAGGAAUUAUUGGAGUUAUCCAGACUACUACAGCA 1440
DB 1381 GAACAUUAUGCAUUGAGUAGGAAUUAUUGGAGUUAUCCAGACUACUACAGCA 1440
QY 1441 GAGAUUCUACUAGAGGAGUUAAGUACGCAAAAUUGGCGUAGUUAUUAUCUCCAGCG 1500
DB 1441 GAGAUUCUACUAGAGGAGUUAAGUACGCAAAAUUGGCGUAGUUAUUAUCUCCAGCG 1500
QY 1501 GAGAGAGUAGGUGUACUUAUGACCGUUAUUUGAGAGUUCAGACAAAGAGAAUUA 1560
DB 1501 GAGAGAGUAGGUGUACUUAUGACCGUUAUUUGAGAGUUCAGACAAAGAGAAUUA 1560
QY 1561 CUACUUAUCUCUGAGAGGUGUACUUAUACAGGAGACAGAGAAUCUGCAUUAUCU 1620
DB 1561 CUACUUAUCUCUGAGAGGUGUACUUAUACAGGAGACAGAGAAUCUGCAUUAUCU 1620
QY 1621 UCAUUGUUAUUGAGAGUUAUUGGCGUUGGAGUACUUGUUAUUAUUAUUG 1680
DB 1621 UCAUUGUUAUUGAGAGUUAUUGGCGUUGGAGUACUUGUUAUUAUUAUUG 1680
QY 1681 UGGAUUAUUGGAGAAACUUGGAAACUUGUUAUUAUUGAGUGUCUACAUUUGCUA 1740
DB 1681 UGGAUUAUUGGAGAAACUUGGAAACUUGUUAUUAUUGAGUGUCUACAUUUGCUA 1740
QY 1741 UACAAUUAUUAUUGAAUUAUUGAGCCAUUUCUUAUUGGCGCAUUAAGGCCAA 1800
DB 1741 UACAAUUAUUAUUGAAUUAUUGAGCCAUUUCUUAUUGGCGCAUUAAGGCCAA 1800
QY 1801 UACAGUGGUGUUGUUAUGACUUAUUAUUAUUGAGAGAGUUAUUGGAGCAUUGAU 1860
DB 1801 UACAGUGGUGUUGUUAUGACUUAUUAUUAUUGAGAGAGUUAUUGGAGCAUUGAU 1860
QY 1861 ACCAGCCAGAAUUAUUAUUAUUAUUGGAGGCGCCCAACCAAGCAAGAUUGAUG 1920
DB 1861 ACCAGCCAGAAUUAUUAUUAUUAUUGGAGGCGCCCAACCAAGCAAGAUUGAUG 1920
QY 1921 CAGUUCUUCUACUGACUUGAGUAGUAGGAGUACAGAAUUAUUCUGUAACGGGC 1980
DB 1921 CAGUUCUUCUACUGACUUGAGUAGUAGGAGUACAGAAUUAUUCUGUAACGGGC 1980
QY 1981 AAUUCUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2040
DB 1981 AAUUCUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2040
QY 2041 GUGGAGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2100
DB 2041 GUGGAGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2100

QY	841	GUANUCAGAGUCCACUAGCAUUCUUUNUGAGAUUGUCCCAACACACAGAUUGGCGG	900
Db	841	GTATCAAGAGATCCACTAGACATCTTTATTATAGATGTGCCACAGCACACAATATGGCGGG	900
QY	901	ACAAAGAUAGUGAGACAUUCUUAUGGACGAACCCACAGAAAGACAAAGCUGUGAATUUGC	960
Db	901	ACAAAGATGGGTGACATTTCTTAGGCGAAGCCGACGAGAAACAAAGCTGTGGATATATGC	960
QY	961	AAGGCGGCAUVGGGACUAGAGUCCUACUCUUCAGUUGUUGGCGGUUCAUUNUAG	1020
Db	961	AAGGTGCGAATGGGACTGAGGATGACGCTCATCTCTCAGCTTTGGGGGTTCACTTTAAA	1020
QY	1021	AGAACACGCGGACUACUACGUCACAGAGAGAGAAAGUGCUUACGGGCAUUCUCAAACA	1080
Db	1021	AGAACCAACGGGTCCTCAATCGACAGCTAGAGAAAGAGTCTTTACAGGCAATCTCCAAACA	1080
QY	1081	UUGAAAUAAAGGUGUCUAGAGGGAAUAGAGAGUUCAAUAGUGUGGAAAAAGGGCAACA	1140
Db	1081	TTGAAAUATTAAGGTCAATAGGGGATGACAGAGGTTCACAATAGGTGGGAAAAAGGGCAACA	1140
QY	1141	GCUUAUUCACAGAAAAACCAACGAGAGAUUGAUAUUCAGCTGUAUUGUGAGUGAGAGAGAA	1200
Db	1141	GCTATATCTCAAGAAAGCAACGAGAGATTTGGTTAGCTCATATGTAGTGGAAAGGAGCAAA	1200
QY	1201	CAGUCGUAUGCUAAGCAUUAUUGUGGCGCAUGGUAUUCUCAAAGAAUUGUAUUGUA	1260
Db	1201	CAGTCAATATGCCGAAGCAATATCTGACATGGTGTGTTTCACAAAGAGATCTGCATGATA	1260
QY	1261	AAAGCAGUAGAGUGUAGUCUAGUUCGUUAUUGGGCAAAUUCAGCGCAUUCAGUCCCAUG	1320
Db	1261	AAAGCAGTTAAGGGGAGACTGATGATTTGTTAACAGGGCAAAATCAGCGGTTAATCCCATG	1320
QY	1321	CAUCAAUCUUNUAAAGCAUUNUUCAGAAAGUCCAAAGUGCUUUUCAAAUUGGGGAUUT	1380
Db	1321	CATCAGCTTTTAAGGCAATTTTCAGAAAGATGCGAAAGTGCTTTTACAGATTTGGGGAATT	1380
QY	1381	GAACAUAVUCGACAUUGUGAGUUGGGAUUGAUUGGGGUAUUAACAGACAUACAUCUCCAAGCA	1440
Db	1381	GAACTATATCGACAGTGTGATGGGAATGGTTGGAAGTATACAGATATATCACTCCAAGCA	1440
QY	1441	GAGAUUGCAUAGAGAGGGGUAAAGAUUCAGAAAUUGGGCGUAGAUUAUUCUCCAGCGG	1500
Db	1441	GAGATGTCAATAGAGAAATTAAGATCAGCAAAATGGGCGTGGATGATCTCCAGACA	1500
QY	1501	GAGAGAGUAGUGUGAGUAGUUAUUGCCGCUUUGAGAGUUCAGACCAACGAGAGAAUUGUA	1560
Db	1501	GAGAGGGTGTGGTTAGCATTCATCGGTTTTGAGAGATTTCCAGACCAACGTGGGAATGTA	1560
QY	1561	CUACUAUCUCUUGAGAGGUGUCUGUAAACACAGGGAACAGAGAAUCUGACAUAUAUCUAC	1620
Db	1561	TTACTATCTCTCGAGAGGGTCAGTGAACACAGGGAAACAGAGAGACTGACATATTACTTAC	1620
QY	1621	UCAUUGUCUAUAGUUGUGGAGUUAUUAUGGCCUUGAGUUCAGUUGUGUUAUAUUAUCUAG	1680
Db	1621	TCATGCTCAATATATGTGGGAGATTAAACGCCCTGTGATCGGTGTGTCAATACCTATCAA	1680
QY	1681	UGGAAUACUAGAAACUUGGGAACUUGUAAAUUUCAGUGGUCUACAGAUUCUCAAUGCUA	1740
Db	1681	TGGATCATCAGAAATTTGGGAAACTGTABAAATTCAATGCTCAGAAATCTGTGCAATGTGTG	1740
QY	1741	UACAAUAAAAUGGAUUTUGAGCCAUUUCAGUCUUCUUAUGUUCUUAAGCCCAUUNAGGCCAA	1800
Db	1741	TACAACAAAATGGAATTTGAAACCAATTCCTTAGTCTTTAGTTAGTCTTAAGAGGCCAA	1800
QY	1801	UACAGUGGCUUUGUAGACUUCUUAUUCCAAACAUAUGGAGAUUUAUUGGCAAUUUGUAU	1860
Db	1801	TAACAGTGAATTTGTCTGAACCTGTATTTCCAAACAAATGAGAGATGACTTGGGACATTTGAT	1860
QY	1861	ACCACCCACAUAAUAAAUUCUUCUUCUCCUUGAGAGCGCCCAACCAAGCAAGUUGAUG	1920
Db	1861	ACCACCCAGATATTAAGCTTCTCTCTTTTGACAGCCGCTCAACCAAGCAAGACAGATG	1920
QY	1921	CAGUUCUCUUCACUGACUGUGAAUUGAGGGGACUACGAGUAGAAUACUUGUAAGGGGC	1980

Db	1921	CAGTTCCTCATTGACTGTGAAATGTGAGGGGANTCAGGANTGAGAAATACCTTGTAAAGGGGC	1980
Qy	1981	AAUUTCUCUAUUVUCAAACUAACAACAAGACCAUAAGAGACUAAACAUUTCUCGAAAGAAU	2040
Db	1981	AATTCCTCGTAATTCACACTACAAACAAGACCACTTAAAGACTTAAACAATTTCTCGAAAAAGAT	2040
Qy	2041	GTUCGGACUCUUAAACUGAAGAACCCGAGUAAGAGCACAUUCUGAGUAGUUCGCGUCUUCUG	2100
Db	2041	GCTGGCACTTAAATTTGAAGAACCCAGATGAAGAACACATCCGAGATGGAGTCCGCTGTCTTG	2100
Qy	2101	AGAGAAUUCUCUANCUNUCUGGGCAAAAGAAUAUAGGAGUAUUGSACCAAGAUUUAAGCAUCAAU	2160
Db	2101	AGAGAAUUTTCATCTCATTGAGTAAAGAAAGACAAAGAAATACGACACGCAATTBAGCATCAAT	2160
Qy	2161	GAACUGAGUAAACCUUUGCGAAAGAGAGAAAGACUUAUUGUAGCUAAUUGGGCAAGAGACUG	2220
Db	2161	GAACTGAGTAACCTTGCMAAAAGGGGAAABAGGCTAATGTGCTAATTTGGGCAAGAGACGTG	2220
Qy	2221	GUGUGUGUAUUGAAACGAAAAACGAAACUCUAGCAUACUACUGACAGCCAGACAGCGAC	2280
Db	2221	GTTGTTGGTAATGAAACAGAAAAACGGGACCTTBAAGCACTTACTGTACAGCACAGACGCAACC	2280
Qy	2281	AAAAAGAUUCGGAUUGGCGCAUCAAUAUUVUGUAUUGUUAAAAAAGACCUUGUUCUAC	2340
Db	2281	AAAAAGAAUUCGAGATGGGCACTCAATTAATGTTGAATAGCTTTAAAAAAGACCTTGTTCAC	2340
Qy	2341	U 2341	
Db	2341	T 2341	

XX	RESULT 8
AA75689	
ID	AA75689 standard; cDNA; 2341 BP.
AC	AA75689;
XX	
DT	11-SEP-1997 (first entry)
XX	
DE	Mutant PB2 protein, ALA7, coding sequence.
XX	
KW	Influenza virus; PB2 protein; charged cluster; master donor virus;
KM	influenza A virus A/LA/2/87; ALA1; ALA2; ALA3; ALA4; ALA5; ALA6;
KM	ALA7; ALA8; attenuation; viral phenotype; temperature sensitivity;; ss.
KM	vaccine; influenza virus A/Memphis/8/80;
XX	
OS	Influenza virus.
OS	Synthetic.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers 28..2307 /*tag= a /product= ALA7
XX	
PN	WO9639179-A1.
XX	
PD	12-DEC-1996.
XX	
PF	03-JUN-1996; 96WO-US08441.
XX	
PR	05-JUN-1995; 95US-0462388.
XX	
PA	(AVIR-) AVIRON.
XX	
PI	Coelingh KL, Parkin NT;
XX	
DR	WPI; 1997-042859/04.
DR	P-PSDB; AAW07711.
XX	
PT	Recombinant influenza virus with mutation(s) in charged cluster regions - esp. temperature sensitive mutation(s), has attenuated phenotype suitable in vaccines for preventing influenza


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QY 1801 UACAGUGGUGUUGUAGACUCUUAUCCAAACAAUAGAGGAGUAGUACUUGGACAUUUUGAU 1860
DB 1801 TAGAGTGATTTGGCAGAACTCTATTCACAAATGAGATGTATCTTGGGACATTTGAT 1860
QY 1861 ACCACCCAGAUAAUAAAACUUCUCCUUCGACCCGCCCAACAAAGCAAAGUAGAU 1920
DB 1861 ACCACCCAGAUAAUAAAACUUCUCCUUCGACCCGCCCAACAAAGCAAAGUAGAU 1920
QY 1921 CAGUUCUCUACGACUGUAGUAGUAGGAGUACGAGAAUAGAUUAUCUUGUAGGAGC 1980
DB 1921 CAGUUCUCUACGACUGUAGUAGUAGGAGUACGAGAAUAGAUUAUCUUGUAGGAGC 1980
QY 1981 AAUUCUCCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2040
DB 1981 AATTCTCCTGTATTCATCACTACAAAGCCACTAAAGAACTMAACAATTCGCGAAAGAT 2040
QY 2041 GCUGGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2100
DB 2041 GCTGGCACTTTAAATGAAAGCCAGATGAAAGCACTCCGAGTGGAGTCCGCTGTCTTG 2100
QY 2101 AGAGAGUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2160
DB 2101 AGAGAGUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2160
QY 2161 GAACUGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2220
DB 2161 GAACUGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2220
QY 2221 GUGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2280
DB 2221 GTGTGGTAATGAAACGAAACGAGGACTCTAGCACTACTTACGACGACGACGACGAC 2280
QY 2281 AAAAGAGUUCGAGUUCGAGUUCGAGUUCGAGUUCGAGUUCGAGUUCGAGUUCGAGUUC 2340
DB 2281 AAAAGAGUUCGAGUUCGAGUUCGAGUUCGAGUUCGAGUUCGAGUUCGAGUUCGAGUUC 2340
QY 2341 U 2341
DB 2341 T 2341

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RESULT 9
AAT75683
ID AAT75683 standard; cDNA; 2341 BP.
XX
AC AAT75683;
Y-

10-SEP-1997 (first entry)
X. Mutant PB2 protein, ALA1, coding sequence.
DE Influenza virus; PB2 protein; charged cluster; master donor virus;
XX Influenza A virus A/LA/2/87; ALA1; ALA2; ALA3; ALA4; ALA5; ALA6;
KW ALA7; ALA8; ALA9; ALA10; ALA11; ALA12; ALA13; ALA14; ALA15; ALA16;
XX vaccine; Influenza virus A/Memphis/8/88; ss.

OS Influenza virus.
XX Synthetic.
XX

Key CDS Location/Qualifiers
FT 28..2307
FT /*tag= a
FT /product= ALA1

XX WO9639179-A1.
XX 12-DEC-1996.
XX 03-JUN-1996; 96WO-US08441.
XX 05-JUN-1995; 95US-0462388.
XX

PA (A/VR-) AVIRON.
XX Coelighn KU, Parkin NT;
XX WPI; 1997-042659/04.
DR P-PDB; AAW07705.
XX
XX Recombinant influenza virus with mutation(s) in charged cluster
PT regions - esp. temperature-sensitive mutation(s), has attenuated
PT phenotype suitable in vaccines for preventing influenza
PS Claim 7; Page -; 39pp; English.
XX
XX The sequences given in 775683-90 encode modified influenza virus PB2
CC proteins, ALA1-ALA8. The modified proteins are generated by replacing
CC certain Arg, Lys and Asp residues in one of 8 charged clusters
CC identified in influenza A virus A/LA/2/87 PB2 protein, with Ala
CC residues. Specifically, the mutations are as follows: ALA1 (residues
CC 2-6) ERIKE -> EAINR, ALA2 (residues 120-124) DYVER -> DAVEA, ALA3
CC (residues 140-144) KIRRR -> KIRAA, ALA4 (residues 187-192) KEKKEE ->
CC KEAEE, ALA5 (residues 339-343) KEKEE -> AAEKE, ALA6 (residues 677-681)
CC (residues 736-740) KRKR -> ARKR. Recombinant influenza viruses which
CC contain these mutations produce attenuated viral phenotypes, useful as
CC master donor viruses in the preparation of immunogenic compositions,
CC e.g. vaccines, for preventing influenza, or a disease associated with
CC influenza infection. Modification of charged cluster residues results
CC in consistent and predictable exhibition of temperature sensitivity.
CC These sequences are not given in the specification and are based on the
CC influenza virus A/Memphis/8/88 given in Genbank M73517.
XX
SQ Sequence 2341 BP; 800 A; 427 C; 576 G; 538 T; 0 other;
Query Match 89.3%; Score 2089.8; DB 18; Length 2341;
Best Local Similarity 71.6%; Pred. No. 0;
Matches 1675; Conservative 509; Mismatches 157; Indels 0; Gaps 0;

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FT /product= ALA2
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 PN 12-DEC-1996.
 XX 03-JUN-1996; 96WO-US08441.
 PF 05-JUN-1995; 95US-0462388.
 XX (AVIR-) AVIRON.
 PA Coelighn KL, Parkin NT;
 PI WPI: 1997-042859/04.
 XX P-PSDB: AAM07706.
 DR
 XX
 PT Recombinant influenza virus with mutation(s) in charged cluster
 PT regions - esp. temperature-sensitive mutation(s), has attenuated
 PT phenotype suitable in vaccines for preventing influenza

Ps Claim 7; Page -; 39pp; English.

CC The sequences given in T75683-90 encode modified influenza virus PB2
 CC proteins, ALA1-ALA8. The modified proteins are generated by replacing
 CC certain Arg, Lys and Asp residues in one of 8 charged clusters
 CC identified in influenza A virus A/LA/2/87 PB2 protein, with Ala
 CC residues. Specifically, the mutations are as follows: ALA1 (residues
 CC 2-6) ERIKE -> EAIAR, ALA2 (residues 120-124) DKVER -> DAVEA, ALA3
 CC (residues 140-144) KIRRR -> KIRAA, ALA4 (residues 187-192) KEKKEE ->
 CC KEAAEE, ALA5 (residues 339-343) KRBER -> AAEEB, ALA6 (residues 677-681)
 CC EDPDE -> EAPPA, ALA7 (residues 699-703) KEDRR -> KEDAA and ALA8
 CC (residues 736-740) KRKRD -> ARKRD. Recombinant influenza viruses which
 CC contain these mutations produce attenuated viral phenotypes, useful as
 CC master donor viruses in the preparation of immunogenic compositions,
 CC e.g. vaccines, for preventing influenza, or a disease associated with
 CC influenza infection. Modification of charged cluster residues results
 CC in consistent and predictable exhibition of temperature sensitivity.
 CC These sequences are not given in the specification and are based on the
 CC influenza virus A/Memphis/8/88 given in Genbank M73517.

XX
 XX
 SQ Sequence 2341 BP; 802 A; 426 C; 575 G; 538 T; 0 other;

Query Match 89.2%; Score 2088.2; DB 18; Length 2341;
 Best Local Similarity 71.5%; Pred. No. 0;
 Matches 1674; Conservative 509; Mismatches 158; Indels 0; Gaps 0;

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DB 2341 T 2341

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KW Influenza A virus A/La/2/87; ALA1; ALA2; ALA3; ALA4; ALA5; ALA6;
KW ALA7; ALA8; attenuation; viral phenotype; temperature sensitivity;
KW vaccine; influenza virus A/Memphis/8/88; ss.
OS Influenza virus.
FX Synthetic.
FH Key
FT CDS Location/Qualifiers
FT 28..2307
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EN M09639179-AL.
PD 12-DEC-1996.
PF 03-JUN-1996; 96MO-US08441.
PR 05-JUN-1995; 95US-0462388.
XX (AVIR-) AVIRON.
XX Coeligh KL, Parkin NT;
XX WPI; 1997-042859/04.
XX DR P-PSDB; AAM07707.
XX PT Recombinant influenza virus with mutation(s) in charged cluster
XX PT regions - esp. temperature-sensitive mutation(s) has attenuated
XX PT phenotype suitable in vaccines for preventing influenza
XX Claim 7; Page -; 39pp; English.
XX
XX The sequences given in T75683-90 encode modified influenza virus PB2
XX proteins, ALA1-ALA8. The modified proteins are generated by replacing
XX certain Arg, Lys and Asp residues in one of 8 charged clusters
XX identified in influenza A virus A/La/2/87 PB2 protein, with Ala
XX residues. Specifically, the mutations are as follows: ALA1 (residues
XX 2-6) ERIKE -> EAIAE; ALA2 (residues 120-124) DKVER -> DAVEA; ALA3
XX (residues 140-144) KIRRR -> KIIAA; ALA4 (residues 187-192) KEKKEE ->
XX KEAAEE; ALA5 (residues 339-343) KRERE -> AAREE; ALA6 (residues 677-681)
XX EDDEE -> EAPPA; ALA7 (residues 699-703) KEDRR -> KEDPA and ALA8
XX (residues 736-740) KRKRD -> ARKRD. Recombinant influenza viruses which
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XX e.g. vaccines, for preventing influenza, or a disease associated with
XX influenza infection. Modification of charged cluster residues results
XX in consistent and predictable exhibition of temperature sensitivity.
XX These sequences are not given in the specification and are based on the
XX influenza virus A/Memphis/8/88 given in Genbank M73517.
XX
XX Sequence 2341 BP; 803 A; 426 C; 575 G; 537 T; 0 other;
XX
XX Query Match 89.2%; Score 2088.2; DB 18; Length 2341;
XX Best Local Similarity 71.5%; Pred. No. 0;
XX Matches 1674; Conservative 509; Mismatches 158; Indels 0; Gaps 0;
QY 1 AGCGAAAGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 60
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XX	15-NOV-2001 (first entry)
DE	Equine influenza virus H3N8 neicaiPB22341 DNA.
XX	
KM	Equine influenza virus; ei; cold adaptation; temperature sensitivity;
XX	vaccine; neicaiPB22341 DNA; PeicaiPB2759 protein; ds.
XX	
OS	Equine influenza virus H3N8.
XX	
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BE	16-FEB-2001; 2001WO-US05048.
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PR	16-FEB-2000; 2000US-0506286.
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PA	(UYP1-) UNIV PITTSBURGH.
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PI	Dowling PW; Youngner JS;
XX	
DR	WP1; 2001-522584/57.
XX	P-PSDB; AAE09026.
XX	
PT	Novel isolated equine influenza virus (wild-type and cold-adapted)
PT	proteins and viruses containing nucleic acid molecules encoding the
PT	proteins, which are useful for protecting animals from influenza virus
PT	infections -
XX	
PS	Claim 2; Page 64-67; 172pp; English.
XX	
CC	The patent discloses cold-adapted equine influenza viruses and
CC	reassortant influenza A viruses comprising at least one genome
CC	segment of such an equine influenza virus, wherein the equine
CC	influenza virus genome segment confers at least one identifying
CC	phenotype of the cold-adapted equine influenza virus, such as
CC	cold adaptation, temperature sensitivity, dominant interference
CC	or attenuation. The viruses are useful for protecting animals
CC	from diseases caused by influenza viruses. They are also used
CC	as vaccines. The present sequence is equine influenza (ei) virus
CC	H3N8 neicai (cold adapted) PB22341 DNA encoding PeicaiPB2759
CC	protein.
XX	
XX	
SO	Sequence 2341 BP; 812 A; 443 C; 564 G; 522 T; 0 other;
QY	Query Match 77.0%; Score 1801.8; DB 22; Length 2341;
	Best Local Similarity 66.1%; Pred. No. 0;
	Matches 1547; Conservative 457; Mismatches 337; Indels 0; Gaps 0
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Qy	1201	CAGUGUAUGACUGAAGCAUAUAUUTGCGCANUGUAUUTUUCACAAAGAAUUGUAUUGA	1261
Db	1201	CATCAATATGCTGAAGCAATAAATTGTAGCCATGAGTGTCTTTCGCAAGAAATTCGATGA	1261
Qy	1261	AAAGCAGUUAAGUGAUCUGAUAUUTCGUUAUAUAGGGCAAAACAGCGAUGUAUCCCAUG	1321
Db	1261	CAGAGAGTTCCAGGGGATTTGAACCTCGTTAATAGAGCAAAATCAGCGCTTGAACCCATG	1321
Qy	1321	CAUCAAACUUTUAAACAUAUUTUCAGAAAGUCCGAAAGUCUUTUCAAUAUUGGGGAU	1381
Db	1321	CATCAACTCTTGAGGCAATTTCCAAAAMAAATGCAAAAAGTCTTTTCAGAAATTGGGGAT	1381
Qy	1381	GAACGUAUACGACAAUGUAUGGGAUUGGGAUUAUUGGGUAUUAACGAGAUCAUCCCAAGCA	1441
Db	1381	GAACCCATCGAACAAATGTATGGGAATGTGAATTAATTTGCTCGACATGACCCCAAGCAC	1441
Qy	1441	GAGAUUGCAUAGAGAGGGUAAGAGUCGCAAAAAGGGCGUAGUAUAUCCACGGCG	1501
Db	1441	GAGATGTCAATTGAGAGAGTAGAGACTGCGCAAAAATGGAGTGTGATGATCTCCAGACT	1501
Qy	1501	GAGAGUAUUGUGUGACUAUAGCCGUGUUTUGAGAGUUCGAGACCAAGAGAAUUGUA	1561
Db	1501	GAGAGAGTGTGTGTGACGATTGACCGTCTTTTAAAGATTCGGGATCAAAAGGGGAAACAT	1561
Qy	1561	CUACAUUUCUCUGAGAGAGGCAUGGAAACAAGGGAAACAGAGAAUUCUAUAUCCUAC	1621
Db	1561	CTACTGTCTCCCTGAAGAGGTCAAGTGAACAAGAGACGAAAGACTGACAAATTAATTTAT	1621
Qy	1621	UCAUCGUAUGAUGUGUGGAGAUUAUAGCCCGUAGUCAGUGUGUGUCAAUAUCCUAUAG	1681
Db	1621	TCATCATCAATGATGTGGGATTTAATGTGTCCGAATCAAGTGTGTGCTAATCTTAATCAA	1681
Qy	1681	UGGACUAUCAGAAACUGGGAAACUGUUAUAUUCAGUGGUCUCAGAAUCCUAACAUCUA	1741
Db	1681	TGGATCATCAAGAACTGGGAAATTGTGAAAAATTCAAATGTCTACAGAGATCCCAATGT	1741
Qy	1741	UACAAUAAAUAUGAAUUTUAGCCCAUUTUAGUCUUAUGCCUAAGCCCAUUAAGGCCAA	1801
Db	1741	TACAAATAGATAGAAATTTGAGCCCATTCAGTCCCTGTGCTCTAGGGCCACACAGAACCA	1801
Qy	1801	UACAGUGGUGUUGUAAGACUCUAUUTUCCAAUAUAGAGAGAGUAUUCUGGGACAUUGAU	1861
Db	1801	TACAGCGGTTTCGTAAGAACCTGTCTTTCAGCAAAATGCGAAGATGATCTTGGAACTTTAT	1861
Qy	1861	ACCAACCCAGUAUAAAACUUCUUCUCCUUGCAGCCGCCGCCACCAAGCAAAUGAUAUG	1921
Db	1861	ACTGCTCAAAATAAATAAACTCTCTCTTTTTCGCTGTCTCTCCGGAAACAGATAGCATG	1921
Qy	1921	CAGUUCUUCACUGACUGUGUAUUGUAGGGGAAACAGAAUAGACAUAUUCUGUAAGGGC	1981
Db	1921	CAGTTCTCTCTTGTACCTGTTAATGTAAAGAGATCGGAAATGAGAGATCTTGTAAAGAGC	1981
Qy	1981	AAUUCUCCUAUUAUUAACUAACAACAACCAACUAUAGAGACUAACAUAUUCUGCAAAAGAU	2041
Db	1981	AATTCCCCAGTTCACACTACAAATAAAGCCACTAAGAGCTCACAGTCTCTCGAAAAAGAT	2041
Qy	2041	GCUGGCAACUUAACUGAAGACCCAGUAAGGCAUAUCUGAGUGAGUCCGUGUUGC	2101
Db	2041	GCAGGTCCGCTTACGTAAAGACCCAGATGAAGGTACGCTGGAGTGAATCTGCTTCTA	2101
Qy	2101	AGAGAGUUCUUAUUCUGGCAAAAGAGUAUGAGAUUGGACAGCAUUAAGCAUUAU	2161
Db	2101	AGAGGTTTCTCATTTTATGAGTAAAGAAACAAGATATGTGCCACAGACTTAAGATCAAT	2161
Qy	2161	GAACUGAGUAACCUUGCGAAAGAGAAAGGCUUAUUGACUAUUGGGCAAGACAGACUG	2221
Db	2161	GAACGTGACAAACTTGCAAAAGGGGAGAAAGCTAATGTGCTAATTTGGGCAAGGGGACGTG	2221
Qy	2221	GUGUGGUAAUUGAAACGAAACCGAACUCUAAGCAUACUUAUCGACAGCCAGACGAGCC	2281

D6	2221	GTTGTTGGTAAATGAAGACGAAACGTGACTCTTCAGCATCTTA	CTTGACAGCCAGCAGCAGCAC	2280
OY	2281	AAAAGAATUCGCAUGGCCAUCACAUAUAGUGGAAUAAGUUAAAA	CGACCUCUUGUUCUAC	2340
		: : : : : : : :		
D6	2281	AAAAGATTCCGATGCGATGCATCATTAAGTGGATTGTAATGTTAA	AAAAACGACCTTGTTCAC	2340
OY	2341	U 2341		
D6	2341	T 2341		
 RESULT 14				
ID	AAZ50977			
XX	AAZ50977	standard; DNA; 1241 BP.		
AC	AAZ50977;			
DT	05-JUN-2000	(first entry)		
XX				
r	wild type equine influenza virus H3N8 PB2-N protein DNA.			
K-	RNA-directed RNA polymerase; wild type PB2-N protein; horse;			
KM	cold-adaptation; reassortant virus; temperature sensitivity; attenuation;			
KW	antiviral; vaccine; prevention; treatment; dominant interference;			
KM	influenza A virus infection; ds.			
XX				
OS	Equine influenza virus H3N8.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	28..1239		
FT		/*tag= a		
FT		/product= "PB2-N protein"		
FT		/note= "Encodes N-terminal portion of PB2 protein"		
FT		/partial		
FT	misc_feature	28..1241		
FT		/*tag= b		
FT		/note= "This region is specifically claimed"		
PN	WO200009702-A1.			
XX				
PD	24-FEB-2000.			
XX				
PF	12-AUG-1999;	99WO-US18583.		
XX				
PR	13-AUG-1998;	98US-O133921.		
XX				
PA	(UYP1-) UNITV PITTSBURGH.			
Y-				
A.	Dowling PW, Youngner JS;			
DR	MPJ: 2000-224339/19.			
DR	P-PsDB; AA770058.			
PT	New cold-adapted equine influenza viruses and reassortant viruses used			
PT	as vaccines for treating influenza infections in animals, particularly			
PT	horses, have a phenotype such as temperature sensitivity or dominant			
PT	interference			
PS	Claim 8, Page 96-99; 127pp; English.			
XX				
CC	The patent discloses experimentally generated cold-adapted equine			
CC	influenza viruses, and reassortant influenza A viruses comprising at			
CC	least one genome segment of the cold-adapted virus, which confers at			
CC	least one identifying phenotype selected from cold-adaptation,			
CC	temperature sensitivity, dominant interference and attenuation.			
CC	These viruses are used in therapeutic compositions e.g. vaccines for			
CC	preventing or treating infections caused by influenza A viruses in			
CC	animals, particularly horses. The present sequence is a DNA			
CC	(nlewtPB2-N1241) encoding N-terminal portion of wild type PB2			
CC	protein (PwCPB2-M04), an RNA-directed RNA polymerase, from equine			
CC	influenza virus H3N8. This sequence is modified to generate			
CC	cold-adapted equine influenza virus.			
XX				

Seq	Sequence	1241 BP	462 A	231 C	292 G	256 T	0 other
Query Match	41.2%	Score	964.2	DB	21	Length	1241
Best Local Similarity	68.0%	Pred.	No. 2,8e-269				
Matches	844	Conservative	224	Mismatches	173	Indels	0
						Gaps	0
QY	1	AGCGAAGACAGGUCAUUUUUAUUCAAUUAUGGAAAGAAUUAAGAAACUACGAGAAUUCUGAUG	60				
DB	1	AGCAAAAGCAGAGTCAATATATATTCATATGTGAAGATTAAGAACTGAGAGATCTTAATG	60				
QY	61	UCCGAGUCUCGCACTUCGCGAGAUUACUAAACCAACGAGUGACCAUUNUGCCCAUAAU	120				
DB	61	TCACATATCCGCAACCCCGAGATCTTAAGAAAACCTAAGTGGACCACTGGCCATATTC	120				
QY	121	AAGAAGUACAUCUAGGAGGCGAGGAAAGACCCGUCACUUAUGAUAUUGAUAUUGAUG	180				
DB	121	AAGAAATACATCATGAGAGACAAGAGAGAACCCCGCATTTGAGATGAAGTGGATVATG	180				
QY	181	GCATVGAANUUCGGAUUAACGCGCAACAAAGAGUAAACAGAAUUGUUVUCCUGAGAGAAU	240				
DB	181	GCATVGAANUUCGGAUUAACGCGCAACAAAGAGATTAAGATTAAGATTAAGATTAAGATTA	240				
QY	241	GAGCAAGGCGCAACUCUACUAGUAAUUAUGAGUAGUAGUAGUAGUAGUAGUAGUAGU	300				
DB	241	GAGCAAGGCGCAACUCUACUAGUAAUUAUGAGUAGUAGUAGUAGUAGUAGUAGUAGU	300				
QY	301	UACCCUUCGCGUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU	360				
DB	301	UACCCUUCGCGUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU	360				
QY	361	CCAAAACUUAACAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	420				
DB	361	CCAAAACUUAACAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	420				
QY	421	CCUUGUACUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	480				
DB	421	CCUUGUACUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	480				
QY	481	GCAGACUUCAGUGCCAAAGAGGCAACAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	540				
DB	481	GCAGACUUCAGUGCCAAAGAGGCAACAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	540				
QY	541	GUGGAGGCCAGAGUACUAAACGUGCGAAUUCGCAUUAUUAUUAUUAUUAUUAUUAUUA	600				
DB	541	GUGGAGGCCAGAGUACUAAACGUGCGAAUUCGCAUUAUUAUUAUUAUUAUUAUUAUUA	600				
QY	601	GAACTTCCAGAGCTGCAAAATTCGCGAAATCAACATTAACAAATTAACAAATTAACAA	660				
DB	601	GAACTTCCAGAGCTGCAAAATTCGCGAAATCAACATTAACAAATTAACAAATTAACAA	660				
QY	661	GUCCGAAACGAGAUUUCUCCGAGUUGCUGUGGAAACAAAGCAGUGUACUUAUUAUUAU	720				
DB	661	GUCCGAAACGAGAUUUCUCCGAGUUGCUGUGGAAACAAAGCAGUGUACUUAUUAUUAU	720				
QY	721	UUGCAUUGACUACAGAAACUUCUGGAAACAGUUAUUAUUAUUAUUAUUAUUAUUAUUA	780				
DB	721	UUGCAUUGACUACAGAAACUUCUGGAAACAGUUAUUAUUAUUAUUAUUAUUAUUAUUA	780				
QY	781	AUUGAUUGUUGAUCAAAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	840				
DB	781	AUUGAUUGUUGAUCAAAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	840				
QY	841	GUUAGCAGAUUCCAUUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	900				
DB	841	GUUAGCAGAUUCCAUUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	900				
QY	901	ACAAGAGUGGAGUACAUUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	960				
DB	901	ACAAGAGUGGAGUACAUUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	960				
QY	961	AAGGUGGCAUUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU	1020				
DB	961	AAGGUGGCAUUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU	1020				

Db	901	ATAAGATGTGTAACATCCTTAAGAGAAATCCAAAGAGAAACAAGCTGTGATATATG	960
Qy	961	AAGCTUGCAATGGACATGAGAGUACAGTUCACCTUCAGUUUUGCGGGUUCACUUUAAG	1020
Dc	961	AAACGAGAAATGGGGTTTAAGAAATTAGCTTCATTCATTCAGCTTTGGTGGATTCACTTTAAG	1020
Qy	1021	AGAAACAACGGAGUCAUCAAGUCAGAAGAGAGAGAAAGUCUACGGGCAUUCUCAAACA	1080
Dc	1021	AGAACAAATGGATCATCAAGTCAAGAGAGAAAGAAATAGTTAAGCGGCAACTTCAAACA	1080
Qy	1081	UUGAAAAAUAAGGAGUCAGAGAGAAACGAGAGUCCAAAGCUGUUGGGAAAAAGGGCAACA	1140
Dc	1081	TTGAAAAATPAGGTGCATPAGAGGCTATPAGAAATTCATPAGGTGCGAAGAGAGACACACA	1140
Qy	1141	GCUAUACUCAGAAAAAGCAACCAAGAGAUUUGAUCUCUGAUUUGGAGUGAAGAGACGAA	1200
Dc	1141	GCAATTTCTCAGAAAGGCAACCGAAGATTTGATTCAATTGATATGTAAGTGGAGAGATGAA	1200
Qy	1201	CAGUGAGUAGCUGAGCAAUUAUUGBGGCCAUUGCAUUUUC	1241
	1201	CAATCAATTGCTGAAAGCAATTAATTTAGCCATGTGTTTTC	1241

Search completed: December 31, 2003, 16:42:50
Job time : 611 secs

[illegible]

QY	1381	GAACAUUUCGACAUAUUGUAGUUGAGAAUUAUUGUGGGUAUUAUCAGACAUGACUAUCCACAGACA	1440
Db	1381	GAUCCCAATCGACAAATGTGAATGGGAATATATTTGGATATATTTGCTGACATGATCCCAAGCAC	1440
QY	1441	GAGUUGUCAAAGAGAGGGGUAAGAGUCAGCAAAAUGGAGCCUAGUAGUAUACUCCAGCGCG	1500
Db	1441	GAGATGTCAATTGAGAGAGGTGAAGTACGACAAAATGGGAAGTGTGATGTCCTCAGACT	1500
QY	1501	GAGAGAUUAUGUGUGAGCAUUGAACCGGUAUUUGAUAUUTUGAGACCAACGAGGAUAUGUA	1560
Db	1501	GAGAGAGTGTGGTGAACATTGACCGTTTTTTAAAGATTTGGGATTCAAAGGGGAAACATA	1560
QY	1561	CUACUAUUCUCCUGAGAGAGUCAGUGAAGAACACAGGGAAACAGAGAAUCUGACAUAUUAUCUAC	1620
Db	1561	CTACTGTCTCCCTGAAGAGGTCTAGTAAACACAGAGAAACGAGAAAGCTGACATTAATTTAT	1620
QY	1621	UGAUUGUAUUGAGUUGGGAGAUUAUUGCCUGAGUUCAGUUGUGUCAAUUAUCUACAG	1680
Db	1621	TCATCATCAATGATGTGGAGATTAATTAATGTCTCCGAATCAGTTGGTCTCAATATCTATCA	1680
QY	1681	UGAUUCAUUCAGAAACUGGAGAAACUGUUAUAUUCAGUGUUCUCAAUUAUCUAUCUA	1740
Db	1681	TGATCATCAAGAAACTGGGAAATTTGTAAAAATTCAAATGTCAACGAGATCCCAATGTTA	1740
QY	1741	UACAAUAAAAUUGAUAUUGAGACCAUUAUUCAGUCUUAUUGUCCUAAGGCCAUUAUGAGGCCAA	1800
Db	1741	TACAAATAGATAGAAATTTGAGCCATCTCCAGTCCCTGTCTCCTTAGGGCCACAGAAAGCCAA	1800
QY	1801	UACAGUGGUGUUGUUGUAGCAUCUAUUCCAACAAAUAGAGAUUAUCUUGGACAUUTUGAU	1860
Db	1801	TACAGCGGTTTCTGTAGAACCCCTGTCTTTCAGCAAAATGGAGATGTACTTGGAAACATTTGAT	1860
QY	1861	ACCAACCAAGUAUAUAAAAUUCUUCUCCUUGAGACGCGCCCAACAAAGGAAAGUAGAUAUG	1920
Db	1861	ACTGCTCAAAATAAATAAACCTCTCTCTTTGGCCGCTGTCTCTCCGGAACAAAGTAGATG	1920
QY	1921	CAGUUCUCUUCACUGACUUGUAGUAGUGAGGGAGUACAGAAUAGUAUAUCUUGUAAAGGCGC	1980
Db	1921	CAGTTCTCTTCTTGACTGTTTAATGTAAAGAGATCGGAAATGAGGATATCTTGTAAAGGCGC	1980
QY	1981	AAUUCUCCUAUUAUUAUCAAACUACAACAACCACUAAAGAGACUAACAUAUUCUGGGAAGAGAU	2040
Db	1981	AATTCGCCAGTGTCAACTACAAATAAAAGGCCACTAAGAGGCTCACAGTCTCTCGGAAAGGAT	2040
QY	2041	GCUGGACACUUAACUGAAGAACCCAGAUAGAAAGGACCAUUCUGGAGUGUGAGUCCGUGUUGC	2100
Db	2041	GCAAGTGCGCTTACTGTAGAAACCCAGATGMAAGTACGGCTGGAGTAGAATCTTGCTGTTCTA	2100
QY	2101	AGAGAUUUCUUAUUCUGGCAAAAGAAUAUAGAGUAUUGACCCAGCAUUAAGCAUCAAU	2160
Db	2101	AGAGGGTTTCTCATTTTAGGTAAAGAAACAAAGAGATATGGCCAGCACTAAGCATCAAT	2160
QY	2161	GAACUAGUAUAAACUUGGCAAAAGAGAAAAAGCCUAUUAUUAUUGGCAAGAGAGACGUG	2220
Db	2161	GAATCTGAGCAAACTTTCGAAAAAGGGGAGAAACCTAATGTGCTAATTTGGCAAGGGGACCTGT	2220
QY	2221	GUGUGUGUAUAGUAAACGAAAAACGGAACUUCUUGGCAUUAUCUGACAGCCAGACAGCGAC	2280
Db	2221	GTTGTTGGTAATGAAACGGAACCGTGAATCTTAGCATCTTACTGACAGCGCAACAGCGAC	2280
QY	2281	AAAAAGAUUCGGAUGGCCAUCAAUAUUAUUGUUAUUAUAAAAAGCAACUUGCUUUAUC	2340
Db	2281	AAAAGGATTTCCGATGGCCATCAATTAGTGTGAATTTGTTAAAAAGCACTTGTGTTCTAC	2340
QY	2341	U 2341	
Db	2341	T 2341	

RESULT 2
US-09-506-286B-47
; Sequence 47, Application US/09506286B
; Patent No. 6482414

[illegible]

Db	661	GTCCGAAAAACAAGTTCCTCCCACTGCTGCGGAGCAAGCAAGTGTATATCAATTGAAGT	720
Qy	721	UTGCACTGACACUACAGAAACATGCTGCGAACAAGTUAACUCCAGTUGAAGAGG	780
Db	722	TTGACATCTGACCTGAGGAACTGCTGGGACAAATGTATACCCCGAGAGGAAATTAGA	780
Qy	781	AAUGAUGAUGUATUCAAAGUCUAAUUAUUGCAGCCAGAGCAUAUGGAGAGCAGCA	840
Db	781	AACGATGACATTTGATCAAAAGTTTAATTATCTCCCGGAACTATGTGAGAGAGCCACA	840
Qy	841	GUAUAGAGAUCCCACTUGGCUUUAUUGAGAUUGGCCACACGACAACAUAUUGCGCG	900
Db	841	GTATCAGACGATCCCATGACATCCCTCTGGAAAATGTGCCACAGTATCAATATGTGGGA	900
Qy	901	ACAAAGAUUGUGACAUUCCUUAAGCAGAAACCCACAGAAAGACAAAGCTUGGAAUAUUGC	960
Db	901	ATPAGAGATGTAGACATCTTATAGCAGAAATCCACAGAGAAACAAGCTGTGGAATATGC	960
Qy	961	AAGGCGCAUUGGACUGAGGAUACGUCUCCUAGUUGUGCGGUGUCCAUUAUAG	1020
Db	961	AAAGCAGCAATGGGGGTAAAGAAATTAGCTCATCTTCAAGCTTTGGTGTGATCACCTTTAAG	1020
Qy	1021	AGAAACACCGAUCUACUGUCAAAGAGAGAAAGAAGUCUUAACGGGAAATCTUCAAACA	1080
Db	1021	AGAACAAATGGATCTCATGCTCAAGAGAGAAAGAAAGATCTTACGGGCAACCTTCAACA	1080
Qy	1081	UUGAAAAAAGAGGUGCAUGAGGAGAAACGAGAGUUCACAAUGUUGGGAAAAAGGCAACA	1140
Db	1081	TTGAAAAATAAAGTGCATGAAGGCTATGTAGAAATTCACAAATGTGTGGAAAGAGCAACA	1140
Qy	1141	GCUAUACUCAGAAAAAGCAACGAGAGAUUGAUUCAGUCUAGUUGAGUGAGAGACGAA	1200
Db	1141	GCCATTTCTCAAAAAGGCAACGAGAAAGATTGATTCAAATTGATGTAAGTGGGAGAGATGAA	1200
Qy	1201	CAGUGAAGGUGAGCAUAUUGUGCCACUGGUUUUUUACAAGAAAGAUUGUAUUA	1260
Db	1201	CAATCAATTGCTGAAGCAATAATTTGTAGCCATGTGTGTCGAAAGAAATGTGATGATA	1260
Qy	1261	AAAGCAGUUAAGGUGAUCUGAUAUUUGGCUUAUUGGGCAAAUUCAGCAUAUCCCAUG	1320
Db	1261	CAAGAGTTCCAGGGCGATTTGAACCTTGTTAATAGACAAATCAGCGCTTGAAACCCATG	1320
Qy	1321	CAUCAAUUUAAGACAUUUUUCAGAGAGUCCGAAAGUGUCUUUUCAAAUUTGGGGAU	1380
Db	1321	CATCAAACTTGAAGGCAATTCAAAAAAGATGCAAAAGTGCTTTCCAGAAATGGGGGATT	1380
Qy	1381	GAACAUUUCGCAAUUGUGAUGGGAUAUGAUAUUGGGUAUUAACAGCAUAUCUACAAGCA	1440
Db	1381	GAACCCATCGCAAAATGTGATGGGAATATTCGAAATATTTGCTGTGACATGACCCCAAGCAC	1440
Qy	1441	GAGAUUGCAUAGAGCGGGUAAAGAGUACAAAAUUGGGCGUAGUAUAUUCACAGCGCG	1500
Db	1441	GAGATGTCATTTGAGAGAGTGTAGAGTCAAGAAATGGGAGTGTGATCTCCAGCACT	1500
Qy	1501	GAGAGAGUAGUGAGGAGCAUUGACCGGUUUUUUGAGAGUUCGAGACCAACGAGAAUUGA	1560
Db	1501	GAGAGAGTGTGTGTGAGAGATTAAGACCGTTTTTAAGATTTGGGATTCAAAAGGGGAAACTA	1560
Qy	1561	CUACUAUUCUCUGAGAGAGUACUGGAAACACAGGAAACAGAGAAACUGACAUUAACUAC	1620
Db	1561	CTACTGTCCCTTGAAAGAGTCACTGTAACAACAAAGAAACGGAAGAACTGACATATTTAT	1620
Qy	1621	UUAUCUGCAUAGUUGUGAGAGUAUAUAGGCCUUGAGUACAGUUGUGUACUAUACUACAG	1680
Db	1621	TCATCTATCAATGATGTGGAGATTTAAATGTGTCGCAATCAAGTGTGTGATCACTTATCA	1680
Qy	1681	UGGAUUCUACAAAACUGGAAAACUGUUAAAAUUCAGUGUCUCAGAAUUCUACAUUCUA	1740
Db	1681	TGATCATCATCAGAACTGGGAAATTTGTGAAATTCATATGTGTACAGAGATTCACACATGTTA	1740
Qy	1741	UACAAUAAAUAUGAAUUTUGAGCCCAUUTUCAGUCUUUAAGUUCUAAAGCCCAUUAAGCCCA	1800
Db	1741	TACATATAAGATVGAATTTGAGCCATTCACAGTCCCTGTGTCTCCATGAGCCACACAGAACCA	1800

QY 1801 UACAGUGGUGUUGUAGACUUAUUCUACAAUUGAGAGUAGUACUUGGACAUUUGAU 1860
 DB 1801 TACAGCGGTTCTGTAAGAACCTGTCTTACGAAATGCGAGATGTAATTGGAACAATTGAT 1860
 QY 1861 ACCACCCGAGTAUAAAACUUCUCCUUCUCCGACCGCCCAACAAAGCAAAAGUAGAU 1920
 DB 1861 ACTGCTCAAAATAAATAAATCTCCCTTTCGCCCTGCTCCGGAACAGATGAGATG 1920
 QY 1921 CAGUUCUCUACUGACUGAGUAGUGGAGAUACAGAAUUGAUAUUCUUGAGAGGAC 1980
 DB 1921 CAGTCTCTTCTTGTGACGTGTAATGTAGAGAGATCGGAAATGAGATCTTGTAGAGGC 1980
 QY 1981 AAUUCUCCUAUUAUUCACUACACAAAGCAACUAGAGACUUAUUCUGAGAAAGAU 2040
 DB 1981 AATTCCCGAGTTCACATCAATTAAGCCATTAAGAGGCTCAAGTCTCTCGAAAGAT 2040
 QY 2041 GCUGGACUUAUACUAGAAACCCAGUAGACCAUCUGAGUGGAGUCGCGUUCUG 2100
 DB 2041 GCAGGTGGCTTACCTGAAAGCCAGATGAGTACGGCTGAGATGTAATCTGCTGTTCTA 2100
 QY 2101 AGAGAUUCCUACUUCUGGCGAAAGAAAGAUAGAGAUAGACCAUUAUAGCAUUAU 2160
 DB 2101 AGAGGTTTCTCATTTTGTAGTAAGAAACAAGATATGSCCAAGCATTAAGATCAAT 2160
 QY 2161 GAACUGAGUAAACUUGCGAAAGAGAAAGGCUAUAUGUACUUAUUGGCGAAAGAGACUG 2220
 DB 2161 GAATGAGCAAACTTGCAAAAGGAGAGAAAGCTAATGTGTAATGCGCAAGGGAAGTGT 2220
 QY 2221 GUGUGUGUAUAGAAACGAAACGAAACUUGACUACUACUACGACGACAGCGAC 2280
 DB 2221 GTGTGGTAATGAAACGGAACGTAAGCTTAGCTAGCAGGCAACAGCGAC 2280
 QY 2281 AAAAGAUUCCGAGUAGCAUUAUUAUGUUAUUAUAAAACGACUUGUUCUAC 2340
 DB 2281 AAAAGATTGCGATGCGCATCAATTAGTGTGTAATGTTTAAACGACCTGTTTCTAC 2340
 QY 2341 U 2341
 DB 2341 T 2341

RESULT 3
 US-09-506-286B-46
 ; Sequence 46, Application US/09506286B
 ; Patent No. 6482414
 ; GENERAL INFORMATION:
 ; APPLICANT: Dowling, Patricia W.
 ; APPLICANT: Youngner, Julius S.
 ; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
 ; FILE REFERENCE: EQ-1-C2
 ; CURRENT APPLICATION NUMBER: US/09/506,286B
 ; CURRENT FILING DATE: 2000-02-16
 ; PRIOR APPLICATION NUMBER: 09/133,921
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/18583
 ; PRIOR FILING DATE: 1999-08-12
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 46
 ; LENGTH: 2277
 ; TYPE: DNA
 ; ORGANISM: Equine influenza virus H3N8
 US-09-506-286B-46

Query Match 74.7%; Score 1749; DB 4; Length 2277;
 Best Local Similarity 66.3%; Pred. No. 0;
 Matches 1510; Conservative 437; Mismatches 330; Indels 0; Gaps 0;

QY 28 AUGGAAAGAAUAAAGAAACUACGGAUUCUGAGUUGCGACUUGCGAGAGAUUA 87
 DB 1 ATGAGAGAAATTAAGAACTGAGAGATCTAATGTCAACATCCCGACCGGAGATTA 60

QY 88 ACAAACCAACAGUGAGCCAUUAUUGCCAUUAUUAAGAAAGUACAUACGAGGACGAGAA 147
 DB 61 ACAAACCAACAGUGAGCCAUUAUUGCCAUUAUUAAGAAAGUACAUACGAGGACGAGAA 120
 QY 148 AAGAACCCGUCACUUGAGUAGAAUUGAGUAGGAGAAUUAUUGCCAUUAUUGCCGAC 207
 DB 121 AAGAACCCGUCACUUGAGUAGAAUUGAGUAGGAGAAUUAUUGCCAUUAUUGCCGAC 180
 QY 208 AAGAGAUUAACAGAAUUGAUUUCUGAGAAUUGAGCAAGGCAAAUCUUAUGAGUAA 267
 DB 181 AAGAGATTAATGAAATGATTTCTGAGAAATGAAACAGGCGCAAAACCTTTGGAGCAA 240
 QY 268 AUGAGAUUGCCGAGUAGUUGCGAUUGGUAUACCUUGGCGUUGACUAGUGUAU 327
 DB 241 ACGAAGATGCTGCTCAACACCGCCTTAATGATATCACTGCGAGTGAATGATGAT 300
 QY 328 AAGAAUUGACCAUUAUGACGUAUCGUUACUUAUUAUUAUUAUUAUUAUUAUUG 387
 DB 301 AAGAAUUGACCAUUAUGACGUAUCGUUACUUAUUAUUAUUAUUAUUAUUAUUG 360
 QY 388 AAGAGAAAGGUUAAACAUUGAAACUUGGCGCCUUGCAUUAUUAUUAUUAUUAU 447
 DB 361 AAGAGTGAATTAATTAACAGGAACTTTGGCCCGCTTCAATTTAGGAATCAAGTCAAG 420
 QY 448 AUACGCGGAAAGUUGACUUAUUAUUCUGUACUAGACCTUACUUGCCAGAGGACAG 507
 DB 421 ATTAAGACGAGAGTGTATTAACCTGCTGACGCGGACCTGAGTCCAAAGAACACAA 480
 QY 508 GAUGUAUUAUGAGUUGUUAUUGCCUUAACGAAUGGCGGCGAGAAUUAUGUGGGA 567
 DB 481 GATGTATATGTAAGATTTTTCCTAAATGAAGTGGAGGCGCAATTTCAATCGGAA 540
 QY 568 UCGCAUUAUUAACAAUUAACAAAGAAAGAAAGAAACUUCAGAGUUGCAAAUUAUUA 627
 DB 541 TCAACATTAATTAATTAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 600
 QY 628 UUGAGUGUUGCGUACUUGUUAAGAGAGAAACUUGCCGAAAGAGAAUUAUUAUUA 687
 DB 601 TTGATGTAGCAATACATGCTAGAAAGAGATGTCGGAAGAAAGAAAGATTTCTCCAGTG 660
 QY 688 GCUGUGGAAACAAAGCUGUUGUUAUUGAAUGUUGACUUGACUUAAGGAAUUAUUG 747
 DB 661 GCTGCGGAAACAAAGCUGUUGUUAUUGAAUGUUGACUUGACUUAAGGAAUUAUUG 720
 QY 748 GAACAGAUUACACUUCAGUGGAGAGAGAGAGAAUUGAUGUUGUUAUUAUUAUUA 807
 DB 721 GAACAAATGTAACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 QY 808 AUUGCAGCAGAGACUUAUGUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 867
 DB 781 ATTGCTGCCGGAACATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 QY 868 UUGGAGAUUGGCGACAGACAGAUUUGCGGAGCAAGAGUUGGAGACUUAUUGGAG 927
 DB 841 CTGGAATGTCGACAGTACACAGATTTGTGAATTAAGATGATGACATCTTAAGAG 900
 QY 928 AACCCAAAGAGAGAGACUUGGAAUUAUUCAGAGGCUAGAGUUGGAGAGUUAUUAU 987
 DB 901 AATCCAAAGAGAGAGACAGCTGTGATATATGCAAAAGCAGCAATGGCGTTAAGAAAT 960
 QY 988 UCAUCCUACUUGUUGGCGGUGUACAUUAUUAAGAAACAGCGAGUACUAGCAAGAG 1047
 DB 961 TCATCATTCAGGCTGTGTGATTAACCTTTAAGAGAAACAGTGATCATCACTCAAGAG 1020
 QY 1048 GAGGAAAGAGUUGUUGCGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1107
 DB 1021 GAAGAAAGAAATGTTACGCGCAACCTTCAAAACATTAATAAGATGATGATGAAGCT 1080
 QY 1108 GAGAGUUCACAUUGGUGGAAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1167
 DB 1081 GAAGAAATTCACAAATGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140

[illegible][illegible]

Db	601	TTGATGTAGTACATACCTCTAGAAAAGAGTGGTCCAAAAACAAGTTCTCCACTG	660
Qy	688	GCUGUGGAAACAAGAGUGUGUACAUGAAGUGUGCAUCUGACAAGAAACUUGCUG	747
Db	661	GCTGGCGGAAACAAGCAGTGTATACATTAAAGTTGGTCACTTCAGGGAAATGCTGG	720
Qy	748	GAAACAAGTUCACATCCACAGUGUGAACAUGAGGAAUGAGUAGTUGAATCAAAAGTUCUAU	807
Db	721	GAACAAATGTACACCCACAGAGAGAAAGTTAGAAAAGATGACATTGATCAAAAGTTTAAT	780
Qy	808	AUUGAGCGCAGAGAGCAUAGUGGAAAGACAGACAGUATGACAGAGAUCCACUAGCAUCUUA	867
Db	781	ATTGTGCCCCGGAAACATATGTAGAGAAAGACGACAGTATCGACAGATCCCTAGCATCCCTG	840
Qy	868	UUGAGAGUUGCCACAGACAACAGAUUGGCGGGACAAGAGUUGUGAACAUUUCUUAAGCAG	927
Db	841	CTGAAAAATGTGCCACAGTACACAGATTGGTGAATAAAGATGTATGATCATCTCAAGCAG	900
Du	928	AAACCAAGAAGAGCAAGCUGUGAAAUUUAUCCAGGCGUACAUUGGACUUGAGAUACAGC	987
Qy	988	UCAUCUCUACUUAUUGGCGGUGUACAUAUUAAGAAACAAGCGGUAUCUAGUCAAGAGA	1047
Db	961	TCATCATTCACGCTTTGGTGGATTCACCTTTAAGAGAAACAATGTGATCATCATGTCAAGGA	1020
Qy	1048	GAGGAGAAGUGUCUUAACGCGACAUUCUUAACAUUGAAAUUAAGGUGUCAUGAGGAGUAC	1107
Db	1021	GAAGAAAGAAAGCTTACCGGCGCAACCTTCAAACTTTGAAATAAGGTCCATGAAGAGGCTAT	1080
Qy	1108	GAGGAGUUCACAUAUGGUGGGGAAAGGGCAACAGCUAUAUCAGAAAAAGCAACAGAGGA	1167
Db	1081	GAAGATTCCAAATGCTCGGAAGAAAGACACAGCCATTTCTCAGAAAGCAACAGAAAG	1140
Qy	1168	UUGAUUUCAGUCGAVUGUGAGUGGAAGAGACGAACAGUCGAUACUGAAAGCAUAUUGUG	1227
Db	1141	TTGATTTCAATTGATAGTAAAGTGGAGAGATGAACAATCAATTGCTGAAGCAATTAATGTA	1200
Qy	1228	GCCAUGUAUUAUUCACAGAAGAUUGUAUUAUAAAGCAUUAAGUGUAGUACUACAUAUUC	1287
Db	1201	GCCATGTGGTGTTCCTCAAGAAAGATTCAGATACAAAGCAAGTTCCGAGCGGATTTTGAACTTC	1260
Qy	1288	GUUAUAAGGCGAAAUCCAGGAGUUAUUAUCCCAUCCAUCAACUUAUUAAGCAUUAUCAGAA	1347
Db	1261	GTTAATAGACAAATCAGCGCTTGAAACCCATGCATCAACTCTTAGGCAATTTCCAAAAA	1320
Qy	1348	GAUCCGAAAGUCUCUUAUUAUUGGGGAAUUGGAACUAUUCGACAAUUGUGAUGGGAUUG	1407
Du	1321	GATGCAAAAGTCCCTTTCCAGAAATGGGGGATTGAACCCATTCGAAATGTGATGGGAATG	1380
Qy	1408	AUUGGGGUAUUAACGAGACUACUCCACAGACAGUAGUACAUAGAGGGGUAAGAGUC	1467
Db	1381	ATTGGAAATATTCCTCGACATGACCCCAAGCAACGAGATGTCAATTGAGAGGTGAGACTC	1440
Qy	1468	AGCAAAAUAGGGGUAUGAAUACUCCACGCGCGGAGAGAGUAUGUGUGUAGCAUUGACCGG	1527
Db	1441	AGCAAAATGCGAGTGGATGAGTACTCCAGCACTGAGAGAGTGGTGGTGAACATTCACCTG	1500
Qy	1528	UUUUUGAGAGUUCGAGCCAAACGAGGAAAUUGUACUAUUCUCUGAGAGGAGUCAGUGAA	1587
Db	1501	TTTTTAAGATTCGGGATTCAAAGGGGAAACAATACTACTGTCCCTCGAAGAGGTCAGTGA	1560
Qy	1588	ACACAGGGAACAAGAAACUGACAUUAACUUAACUUGUGUACAUUGUGGAGAUUAU	1647
Db	1561	ACACAGGAAACGAAAGCTGCAATTAATTTATCATATCATATGATGTGGAGATTAAT	1620
Qy	1648	GGCCUGAGUCAGUGUGUGUCUAUAUCUAUUCAGUGAGUACUACAGAAACUGGAAACUGUU	1707
Db	1621	GGTCCCGAATCAGTGTGGTCAATCTTAATCAATGATCATCAGGAACCTGGAAATTTGTG	1680
Qy	1708	AAAAUUCAGUGUCUACAGAUUCUACAUGCUAUAUAAAAUUGAAUUGAGCCCAUUT	1767

Db	1681	AAATTCATATGTCACAGATCCCAATATGTTATACAAATAGATAGAAATTTGAGCCATTTC	1740
Qy	1768	CAGCTUUUAAUUTCUUAAAGCCAUUAGAAGGCCAAUACAGUGUGUUUUUUDAGACUUCUAAUUC	1827
Db	1741	CAGTCCCTGTGATCCCTTAAGGCGCACAGAAAGCCAAATACAGCGGTTCCTGTAAAGAAACCTGTGTT	1800
Qy	1828	CAACAAAUAGAGGAGUAGUACUUGGAGACUUDUGAUAACCAACCCAGAUAAUAAAACUUCUCCC	1887
Db	1801	CAGCAAAATGCGAGATGTACTTGAAACATTTGATATCTCTCAAAATATATAAATCTCTCCCT	1866
Qy	1888	UUUUCAGCCGCCCCCAACAAAGCAAAAGUAGAUAGUUCUUCUACUAGACUAGUAGUUG	1947
Db	1861	TTTTCGCGCTGCTCTCTCCGGAACAGATAGATGATGATCTCTTCTTGACTGTAAATGTA	1920
Qy	1948	AGGGGATUCGGAUAGAGAUAACTUGUAAGGGGCAUUCUUCUUAUUAUUAACUACAAAG	2007
Db	1921	AGAGGATCGGGAAATGAGAGATATCTGTAAAGAGGCAATTCGCCAGTGTCAACTAATAA	1980
Qy	2008	AGCAUAUAGAGACUAAACAAUUCUUGGAAAGAGUGUGGCAACUUUAACUAGAACCCAGAU	2067
Db	1981	GCCACTTAAGAGGCTCAACAGTCTCTCGAAAAGATGACAGGTGCGCTTACTGAAGACCCAGAT	2040
Qy	2068	GAAAGCACAUCUGGAGUGAGUCCGCTUUGUUCUGAGAGAUUCCUACAUUCUGGCAAAAGAA	2127
Db	2041	GAAAGTACGCGCTGAGATAGAAATCTGCTGTTCTAAGAGGGTTTCTCATTTTAAGTAAAGAA	2100
Qy	2128	GAUAGAGAUUAGGACACGACAAUUAAGCAUACUAGACUAGUAAACUUGCGAAAGAGAA	2187
Db	2101	AACAAAGATATATGCGCCACAGACATTAACATCAATGAACTGAGCAAACTTGCACAAAGGGGAG	2166
Qy	2188	AAGCUAAUUAUACUAAUUAUUGGGCAAGAGAGUGUGUUAUUAAGAAACGAAACGGAAAC	2247
Db	2161	AAAGCTATATGTCTTAATTATGGACAAAGGGAGCGTGTGTGTGTAATGAACCGAAACGTGAC	2220
Qy	2248	AAAGCAUACUUAUCUGACAGCCACGACACGCAACCAAAAGAUUCCGAGUGCCCAUACAU	2304
Db	2221	TCTATGACTACTTACTGACACGACGACGACGACGCAAAAGAAATTCGATGCGCATCAAT	2277
RESULT 5			
US-09-506-286B-13			
Sequence 13, Application US/09506286B			
Patent No. 6482414			
GENERAL INFORMATION:			
APPLICANT: Dowling, Patricia W.			
APPLICANT: Youngner, Julius S.			
APPLICANT: The University of Pittsburgh, of the Commonwealth			
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES			
FILE REFERENCE: EQ-1-C2			
CURRENT APPLICATION NUMBER: US/09/506,286B			
CURRENT FILING DATE: 2000-02-16			
PRIOR APPLICATION NUMBER: 09/133,921			
PRIOR FILING DATE: 1998-08-13			
PRIOR APPLICATION NUMBER: PCT/US99/18583			
PRIOR FILING DATE: 1999-08-12			
NUMBER OF SEQ ID NOS: 108			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 13			
LENGTH: 1241			
TYPE: DNA			
ORGANISM: Equine influenza virus H3N8			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (28) ..(1239)			
US-09-506-286B-13			
Query Match			
Best Local Similarity 41.2%; Score 964.2; DB 4; Length 1241;			
Matches 844; Conservative 224; Mismatches 173; Indels 0; Gaps 0;			
Qy	1	AGCGAAGACGAGUUAUUUAUUAUUAUUGGAAAGAAUUAAGAAACUACGGAUUCGAG	60
Db	1	AGCAAAAGCGAGGTCTAAATATATATTAATATGAGAGAAATAAAGAACTGAGAGATCTAATG	60

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QY 61 UCGAGUUCGCAUCUCGCGAGAUUACUAAACAAACCAAGGAGCCAUUAGGCCAUUAU 120
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Db 61 TCACAAATCCCGCAGCCCGAGATCTAAACAAAACCTCTGTGGACCAATGGCCATATTC 120
QY 121 AAGAAUGUACAUCAGGAGGAGCAGAAAAGAACCCGUCACUUGAGUAGAUUAGU 180
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Db 121 AAGAAATACACATGAGAGAGACAAAGAGAAAGAACCCGACCTTGAGAGAAAGTGAATG 180
QY 181 GCAUUGAAUUAUCCGAAUUAACCGCAGACAGAGAUAAACAGAAUUAUUCUGAGAGAAU 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GCATGAAATATCCCAATTAACAGCAGATTAAGAGATTAATGAAATGATTCCTGAGAGAAAT 240
QY 241 GAGCAAGGGCAAAUCUUAUGAGAUAAAUAGUGAUUCCGAGUAGUUGAGUAGU 300
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Db 241 GAACAGGGGCAAAACCTTTGGAGCAAAACCAACATCTGGCTCAGACCCGTAATGTAT 300
QY 301 UCAACUUGGUGUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 360
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Db 301 TCACCTCTGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 CCAAAAUUCUACAAACCUUAUUAUUGAGAAAGUAGUAGUAGUAGUAGUAGUAGU 420
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Db 361 CCAAAAGTCTACAAAATTTATTTGAAAGTTGAAAGTTAAACACGGAACCTTTGGC 420
QY 421 CCUGUCCAUUUUAGAAACCAAGUCAAUUAACCCGAGAGUAGUAGUAGUAGUAGU 480
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Db 421 CCGGTCATTTTGAATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 480
QY 481 GCGAGACUUCAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 540
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Db 481 GCGAGACUUCAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 540
QY 541 GUGGAGGCGCAGAUUACUUAAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 600
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Db 541 GTGGAGGCGCAAAATTTCTAATGAGATGCAAACTAACTAACTAACTAACTAACTAA 600
QY 601 GAACTUCAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 660
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Db 601 GAACTUCAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 660
QY 661 GUCCGAGAAACGAGAUUUCUCCAGUUGUGUGAGUAGUAGUAGUAGUAGUAGU 720
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Db 661 GTCCGAGAAACGAGAUUUCUCCAGUUGUGUGAGUAGUAGUAGUAGUAGUAGU 720
QY 721 UUCGACUUGACUACAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 780
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Db 721 TTTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 AAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 840
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 781 AAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 840
QY 841 GUUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 900
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Db 841 GATACGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 900
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Db 901 ATTAAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 960
QY 961 AAGGUGCAUUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1020
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Db 961 AAGGUGCAUUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1020
QY 1021 AAGAAAGCGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1080
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Db 1021 AAGAAAGCGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1080
QY 1081 UUGAAAUUAUUGGUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1140
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Db 1081 TTAAATTAATGAGTGAAGGCTATGAAAGAAATTCACAAATGATGATGATGATGAT 1140

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QY 1141 GCUUAUUCUAGAAAGCAACGAGAUUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1200
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Db 1141 GCCATCTCAGAAAGCAACGAGAUUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1200
QY 1201 CAGUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1241
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Db 1201 CAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1241
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RESULT 6
US-09-762-861B-13
; Sequence 13, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Bowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PQS (formerly HK2-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 1241
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (28)..(1239)
; OTHER INFORMATION:
US-09-762-861B-13

Query Match      41.2%; Score 964.2; DB 4; Length 1241;
Best Local Similarity 68.0%; Pred. No. 2.1e-287;
Matches 844; Conservative 224; Mismatches 173; Indels 0; Gaps 0;

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Db 1 AGCGAAACGAGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 60
QY 61 UCGAGUUCGCAUCUCGCGAGAUUACUAAACAAACCAAGGAGCCAUUAGGCCAUUAU 120
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Db 61 TCACAAATCCCGCAGCCCGAGATCTAAACAAAACCTCTGTGACCAATGGCCATATATC 120
QY 121 AAGAAUGUACAUCAGGAGGAGCAGAAAAGAACCCGUCACUUGAGUAGUAGUAGU 180
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Db 121 AAGAAATACACATGAGAGAGACAAAGAGAAAGAACCCGACCTTGAGAGAAAGTGAATG 180
QY 181 GCAUUGAAUUAUCCGAAUUAACCGCAGACAGAGAUAAACAGAAUUAUUCUGAGAGAAU 240
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Db 181 GCAATGAAATATCCCAATTAACAGCAGATTAAGAGATTAATGAAATGATTCCTGAGAGAAAT 240
QY 241 GAGCAAGGGCAAAUCUUAUGAGUAAAUAGUGAUUCCGAGUAGUUGAGUAGUAGU 300
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Db 241 GAACAGGGGCAAAACCTTTGGAGCAAAACCAACATCTGGCTCAGACCCGTAATGTAT 300
QY 301 UCAACUUGGUGUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 360
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Db 301 TCACCTCTGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 CCAAAAUUCUACAAACCUUAUUAUUGAGAAAGUAGUAGUAGUAGUAGUAGUAGU 420
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Db 361 CCAAAAGTCTACAAAATTTATTTGAAAGTTGAAAGTTAAACACGGAACCTTTGGC 420
QY 421 CCUGUCCAUUUUAGAAACCAAGUCAAUUAACCCGAGAGUAGUAGUAGUAGUAGU 480
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Db 421 CCGGTCATTTTGAAGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 480

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[illegible][illegible]


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; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 1232
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-22

      ery Match      40.2%; Score 941.4; DB 4; Length 1232;
      Best Local Similarity 64.1%; Pred. No. 2.3e-280;
      Matches 789; Conservative 261; Mismatches 181; Indels 0; Gaps 0;

QY 1111 GAGUUCACAUUGGUGGAAAGGCGACAGCUUUAUCUAGAAAGCAACGAGAGUUG 1170
DB 2 GAATTACAAATGCTCGGAAAGAGCAACAGCCATTCTCAGAAAGCAACGAAAGATTG 61
QY 1171 AUVGAGCUAUGUGAGUGAGAGAGCAAGUGUGAUCUGAAAGCAUUAUUGUGCC 1230
DB 62 ATTCAATTGATAGTAAGTGAGAGAGTAAGCAATCTTGAAAGCAATTTGATAC 121
QY 1231 AUVGUAUUVUCCAGAGAGAUUVUUAUAAAGAGUAGAGUGAUCUGAUVUUCGU 1290
DB 122 ATGGTGTTTCCAGAGAAATTTGCATGATTAAGAGAGATTGAGGGGATTGAACTTGG 181
QY 1291 AAUAGGGCAAUUCAGGAGUAGAUUCCCAUGCAUCUUTUUAAGCAUUTUUCAGAGAU 1350
DB 182 AATAGAGCAAAATCAGGCTTGGAACCCCATGATCAACTCTTGAGGCAATTTCCAAAAT 241
QY 1351 GCGAAAGUCUUUUUCAAUUGGGGAAUUGAAUUAUUAUUAUUGGAAUUGAU 1410
DB 242 GAAAAAGTCTCTTCCAGAAATTTGGGGATTTGAACCCATGCAAAATGTGATGAGATT 301
QY 1411 GGGGUAUUVACAGACAGUAGUCCCAAGCAGACAGAGUAGUAGAGGGGUAAGUGUAGC 1470
DB 302 GGAATATTCTCGACATGACCCCAAGACACCGAGATGTCATTGAGAGAGTGAATGAC 361
QY 1471 AAAAUGGGCGUAUUAUUAUCCAGCGGAGAGAGAGUAGUGUGAGCAUUGACCGGU 1530
DB 362 AAAAATGGGAGTGAGTACTCAGACCTGAGAGAGTGTGTGAGCATTTGACCGTTT 421
QY 1531 UUGAGAGUUGAGACCAAGAGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1590
DB 422 TTAAAGATTTGGGATCAAAAGGGGAAACATATCTGTCCCTGAAAGGTCGTAAACA 481
QY 1591 CAGGAAACAGAGAAACUGACAAUUAUCUUAUCUUAUUGAGUGAGAGUUAUUGGC 1650
DB 482 CAAGGAAACGAAAGAGTGAACAATTAATTATTCATCATCATATGATGGAGATTAATGT 541
QY 1651 CCUGAGUAGUGUGUGUUAUUAUCUUAUUGAGUAGUAGAAACUGGAAACUGUUA 1710
DB 542 CCCGATATCGTGTGCTCAATCTTATCAATGATCATCAGGAACTGGGAAATTTGTGAA 601
QY 1711 AUVGAGCUAUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1770
DB 602 ATTCAATTGATAGTAAGTCCACAAATGTTATCAATTAATTAATTAATTAATTAATTA 661
QY 1771 UCUUUAUUGUAGAGGCAUUAUAGAGGCAUUAUAGUGUGUGUAGUAGUAGUAGUAG 1830
DB 662 TCCCTGCTGCTGAGGCGACAGAGAGCAATATACAGGCTTTGTAAGAACCTGTTTCA 721
QY 1831 CAAUAGAGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1890

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DB 722 CAAATGCGAATGATTAATCTGAAACATTTGATGATGCTCAATAATTAATAAATCTCCCTTT 781
QY 1891 GCAGCCGCCCCCAAGAAAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1950
DB 782 GCGCTCTCTCTCGAGAAAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 841
QY 1951 GGAUCAGAAUAGAAUUAUCUUAUAGGGGCAUUVUCCUUAUUAUUAUUAUUAUUAUUA 2010
DB 842 GATCGGAAUAGAGATTAATCTGTAAGAGGCAATTTCCCAAGTGTCAATCAATTAAGCC 901
QY 2011 ACUAAAGACUAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2070
DB 902 ACTAAGAGCTCAACAGTCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 961
QY 2071 GGCACAUUCUGAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 2130
DB 962 GGTACGCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1021
QY 2131 AGGAGAUUAGGACCAAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2190
DB 1022 AAGGATATGCGCCAGCACTAAGCACTAATGAATGAATGAATGAATGAATGAATGAAT 1081
QY 2191 GCUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2250
DB 1082 GCTAATGTGTAATTTGGGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1141
QY 2251 AGCAUAUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2310
DB 1142 AGCATCTTACTGACAGCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1201
QY 2311 UGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2341
DB 1202 TGAATTTGTAATAAAGCAAGCTGTTCTACT 1232

RESULT 10
US-09-762-861B-22
; Sequence 22, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1232
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-762-861B-22

Query Match      40.2%; Score 941.4; DB 4; Length 1232;
Best Local Similarity 64.1%; Pred. No. 2.3e-280;
Matches 789; Conservative 261; Mismatches 181; Indels 0; Gaps 0;

QY 1111 GAGUUCACAUUGGUGGAAAGGCGACAGCUUUAUCUAGAAAGCAACGAGAGUUG 1170
DB 2 GAATTACAAATGCTCGGAAAGAGCAACAGCCATTCTCAGAAAGCAACGAAAGATTG 61
QY 1171 AUVGAGCUAUGUGAGUGAGAGAGCAAGUGUGAUCUGAAAGCAUUAUUGUGCC 1230
DB 62 ATTCAATTGATAGTAAGTGAGAGAGTAAGCAATCTTGAAAGCAATTTGATAC 121

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Db 543 CCCCAGTACAGTGTGGTCAATTACTATCAATGATCAATCAGGAACCTGGGAAATTGTGAA 602

Qy 1711 AATUCAGGUCUCUCAGAAUUCUCAAUUGCUAAUCAAUAAUAGAAUUTGAGCCAUUUCAG 1770

Db 603 ATTCAATGATGTCACAGAGATCCCAATGTAATCAATTAAGATGAAATTTGAGCATTTCCAG 662

Qy 1771 UCUUUAUUCUCUAAAGGCCAUUAGAAGCCAAUUCAGUUGGUCUUUGUUAUGAGUCUUAUUCGA 1830

Db 663 TCCCTGGTCCCTTAGGGCCCAACGAAAGCCAAATACAGCGGTTTGTAAGAAACCTGTGTTG 722

Qy 1891 CAAUUGAGGAGUAVUCUUGGAGCAUUCUUGAUAACCAACCAAGUAUAUAAACUUCUUCUCCUU 1890

Db 723 CAAATGCGAGATGTAATCTTGAAACATTTGATTAATCTGCTCAAAATTAATAAACTCCTCCCTTT 782

Qy 1891 GCAGCCGCCCCCAACGAAGGAAAGUAGAAUUGCAGUUCUCUCUACUGACUGAGUAGUAGG 1950

Db 783 GCGCGTGTCTCCTCCGGAACAGAGTAGAGATGCAAGTTCTTCTTGAACGTGTAATGAAGA 842

Qy 1951 GGAUACAGAAUAGAAUACUUCUUAUAGGGGCAUUCUUCUUAUUAUUCACUACAAAGAAC 2010

Db 843 GGATCGGGAATGAGGATTAATCTTGTAAGAGGCAATTCGCCAGTGTTCAACTACAAATAAGGC 902

Qy 2011 ACUAAAGAGACUAAAUUCUUGGAAAGAAUUGCUGGACUCUUAUCUAAUCUAGAACCCAGUAGA 2070

Db 903 ACTTAAGAGGCTACAGCTCCTCGAAAGATGACAGTGCGCCTTAATCTAAGAACCCAGATGAA 962

Qy 2071 GGCAUUCUUGGAGUAGUCCGUCUUCUGAAGAGAUUCUUCUACUUCUUGGGCAAAAGAAU 2130

Db 963 GGTACGGCTGAGATGAATCTGTGTTTAAGAGGGGTTTCTCATTTTAAAGTAAGAAAC 1022

Qy 2131 AGGAGAUUUGACACGACCAUUAAGCAUUAUUAAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2190

Db 1023 AAGAAATATGCGCCAGACACTTAAGCAATGAATGAAGAAACTTGCAAAAGGGGAGAA 1082

Qy 2191 GCUAAUUGUACUUAUUGGGGCAAGGAGACGUGUGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUA 2250

Db 1083 GCTAATGTCTTAATTTGGGCAAGGAGACGTGTGTTGTAATGAAGAAACGTGACTCT 1142

Qy 2251 AGCAUACUUAUCGACAGCCAGACGACCCAAAGAAUUCGAGUUGCCAUUAUUAUUAUUAUUAU 2310

Db 1143 AGCATACTTAAGTGAAGCCAGACAGGACCAAAAGGATTCGATGGCCATCAATTAAGTGT 1202

Qy 2311 UGAUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2341

Db 1203 TGAATGTGTTAAAAACGACCTGTGTTCTACT 1233

P- "LT 12

1-762-861B-19

-sequence 19, Application US/09762861B

Patent No. 6579528

GENERAL INFORMATION:

APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher Education

APPLICANT: Education

APPLICANT: Downing, Patricia W.

APPLICANT: Youngner, Julius S.

TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

FILE REFERENCE: EO-1-CI-PUS (formerly HK2-033CPUS)

CURRENT APPLICATION NUMBER: US/09/762, 861B

CURRENT FILING DATE: 2001-02-13

PRIOR APPLICATION NUMBER: PCT/US99/18583

PRIOR FILING DATE: 1999-08-12

PRIOR APPLICATION NUMBER: 09/133,921

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn version 3.1

SEQ ID NO 19

LENGTH: 1233

TYPE: DNA

ORGANISM: Equine influenza virus H3N8

FEATURE:

NAME/KEY: CDS

LOCATION: (3)..(1196)

OTHER INFORMATION:
US-09-762-861B-19

US-09-762-861B-15

Query Match	40.2%	Score 941.4;	DB 4;	Length 1233;
Best Local Similarity	64.1%	Pred. No. 2.3e-280;		
Matches 789;	Conservative 261;	Mismatches 181;	Indels 0;	Gaps 0;

[illegible]

Db 963 GGTACGGCTGAGTAGATCTGCTGTTCTAAGAGGGTTTCATTTAGTAAAGAAAC 1022
Qy 2131 AGGAGAUUAGACCGACCAUUAAAGCAUAAUCUGAGUAACTUUGCCGAAAGAGAAAAG 2190
Db 1023 AAGAGATATAGGCCAGCACTAAGCATCATGAACTGAGCAAACTTGCAAAAAGGAGAAA 1082
Qy 2191 GGUAAUUGUACUAAUUGGCGAAGAGACGUGUGUUGUUAUAGAAACGAAAACGAAACUCU 2250
Db 1083 GCTAATGCTTAATTTGGGCAAGGGGACGTGTGTGTGTAATGAAAACGAAACGTACTCT 1142
Qy 2251 AGCAUACUACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2310
Db 1143 AGCATATCTTACTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1202
Qy 2311 UGAUUAUU 2341
Db 1203 TGAATTGTTTAAUU 1233
-TIT 13
-Sequence 15, Application US/09506286B
Patent No. 6482414
GENERAL INFORMATION:
APPLICANT: Dowling, Patricia W.
APPLICANT: Youngner, Julius S.
TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth
FILE REFERENCE: EO-1-C2
CURRENT APPLICATION NUMBER: US/09/506,286B
PRIOR FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: 09/133,921
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/18583
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 15
LENGTH: 1214
TYPE: DNA
ORGANISM: Equine influenza virus H3N8
US-09-506-286B-15
Query Match 40.2%; Score 940.4; DB 4; Length 1214;
Best Local Similarity 68.0%; Pred. No. 4.6e-280;
Matches 825; Conservative 218; Mismatches 171; Indels 0; Gaps 0;
28 AUGGAAAUAAUAAAGAAACUACGGAUUCUGAUGUCGACUCCGACGACGAGAUACUA 87
1 ATGGAGAAATTAATAAGAACTGAGAGATCTTAATGTCAATCCCGACCCGAGATCTA 60
Qy 88 ACAAACCAACACGACGACCAUUAUUGGCAUUAUUAAGAAUACACUACGAGGAGAGAA 147
Db 61 ACAAACCAACACGACGACCAUUAUUGGCAUUAUUAAGAAUACACUACGAGGAGAGAA 120
Qy 148 AAGAAACCGGACUUAUGAUGAAUUGAUGGCAUUAUUAUUGGCAUUAUUGGCAUUAUUG 207
Db 121 AAGAAACCGGACUUAUGAUGAAUUGAUGGCAUUAUUAUUGGCAUUAUUGGCAUUAUUG 180
Qy 208 AAGAGAAUAAAGAAUUAUUCUGAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 267
Db 181 AAGAGAAUAAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 240
Qy 268 AUGAGUAGUGCGGACUUGGACUUGUUGAUGUUAUUAUUAUUAUUAUUAUUAUUAUUAU 327
Db 241 AUGAGUAGUGCGGACUUGGACUUGUUGAUGUUAUUAUUAUUAUUAUUAUUAUUAUUAU 300
Qy 328 AGAAUUGACCAUUGACAAUGACGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 387
Db 301 AGAAUUGACCAUUGACAAUGACGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 360
Qy 388 AAAGUCGAAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 447

Db 361 AAATGAAAGATTAAACACGGAACCTTTGGCCCGCTTATTTAGAAATCAAGTCAAG 420
Qy 448 AUAACCGGAAAGUUGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 507
Db 421 AUAACCGGAAAGUUGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 480
Qy 508 GAUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 567
Db 481 GATGTGATCAATGGAAGTTGTTTCCCAATGAAGTGGGACCGAATTTCAATCCGAA 540
Qy 568 UUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 627
Db 541 TCACATCTTAACAAATTAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 600
Qy 628 UUGAUGUGUGGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 687
Db 601 TTAGATGTACATATACATGATGAAAGAGATTTGGTCCGAAACAAAGATTCCTCCAGTG 660
Qy 688 GUGUGGAAACAAAGACUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 747
Db 661 GCTGGCGGAAACAAAGCAGTGTATCATTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTG 720
Qy 748 GAACAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 807
Db 721 GAACAAATTTACACCCAGAGAGAGAAAGTGAAGAAAGATACATTTGATCAAGTTTAA 780
Qy 808 AUUGACCGGACGAGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 867
Db 781 ATTGCTGCGGAAACAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy 868 UUGAUGUUGGCAACAGACACAGUUGGCGGACAAAGAUUGGACAUUUCUAGGACG 927
Db 841 CTGGAATTTGCGACAGTACAGATTTGGTGAATTAAGATGCTTGAACATCTTAAAGCAG 900
Qy 928 AACCCACAGAAAGACAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 987
Db 901 AATCCACAGAGAAACAGTGTGATATATGCAAAAGCAGACAAATGGGTTAAAGATTA 960
Qy 988 UCAUCCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1047
Db 961 TCATCATTTACGCTTTGGTGGATTCACCTTTAAGAGAAAGATGATCATGATCAAGAGA 1020
Qy 1048 GAGGAAAGACUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1107
Db 1021 GAAGAAGAAATGCTTACGGGCAACCTTCAAACTTGAATTAAGATGATGAAGGCTAT 1080
Qy 1108 GAGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1167
Db 1081 GAAGAATTTCAATGTTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy 1168 UUGAUGUGUGGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1227
Db 1141 TTGATTTCAATTTAGTAAAGTGGAGAGATGAACATCAATTCCTGAAGCAATTAATGTA 1200
Qy 1228 GCCAUGGUUUUUU 1241
Db 1201 GCCATGATGTTTTC 1214
RESULT 14
US-09-762-861B-15
Sequence 15, Application US/09762861B
Patent No. 6579528
GENERAL INFORMATION:
APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
Education
APPLICANT: Dowling, Patricia W.
APPLICANT: Youngner, Julius S.
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
FILE REFERENCE: EO-1-C1-PUS (formerly HKZ-033CUS)
CURRENT APPLICATION NUMBER: US/09/762,861B
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: PCT/US99/18583

; PRIOR FILING DATE: 1999-08-12
 ; PRIOR APPLICATION NUMBER: 09/133,921
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 15
 ; LENGTH: 1214
 ; TYPE: DNA
 ; ORGANISM: Equine influenza virus H3N8
 US-09-762-861B-15

Query Match 40.2%; Score 940.4; DB 4; Length 1214;
 Best Local Similarity 68.0%; Pred. No. 4,6e-280;
 Matches 825; Conservative 218; Mismatches 171; Indels 0; Gaps 0;

QY 28 AUGGAAAGAAUAAAAGAAUUCUGAUGUGGCGACUCGCGGAGUACUA 87
 DB 1 ATGGAGAGATTAAGAAAGATGAGAGATCTAATGTCACATCCGACCGCGAGATCTA 60
 88 AAAAAACGACAGUGGACCAUUGGCGCAUUAUUAGAAGUACAUCAGGAGGACAGAA 147
 61 AAAAAAATACTGTGGACCAATGCGCATATCAAGAAATACATCAGGAAAGACAGAG 120
 LW 148 AAGAACCCGUCACUUGAGUAGAAUUGAGUAGGCAUAGAAUUAUCCGUAUACGCCAC 207
 DB 121 AAGAACCCGACCTTAGATGAAGTGATGATGCGCATGAAATATCCAAATTACAGAGAT 180
 QY 208 AAGAGAAUAAACAAAUUUCUGAGAGAAUAGACAGGCGCAACUCUUGAGUAAA 267
 DB 181 AAGAGATTAATGAATATCTCTGAGAGAAATGAACAGGCGCAAAACCTTTGAGACAAA 240
 QY 268 AUGAGUAGUCCCGAGUAGGAGUUGUGUAGUUAUACAUCUGGCGUGAGUAGUAGAAU 327
 DB 241 ACGAGAGATCTGTGCTGACAGCCGCTAATGATATCACTCTGCGCATGACATGATGAAAT 300
 QY 328 AGAAUAGACCAUAGACAGUUGGCUUUAUCCAAAUAUCCAAACAAUUAUUGUAG 387
 DB 301 AGGAATGACCAACAGAGACACATTCATATCCAAATCTACAAACCTTTTGGAA 360
 QY 388 AAGUGGAAAGUUAAAACUUGAACCUUUGGCGUGGCUUUAUUAAGAAACCAAGUAAA 447
 DB 361 AAGGTTGAAGATTAAACACGGAACCTTTGGCCCGTTATTTAGAAATCAAGTCAAG 420
 QY 448 AUAAGCGGAGAGUUGACAUAUAAUUCUGUACUAGACACUUGCGACAGAGAGACAG 507
 DB 421 ATTAAGACGAGAGATTGATTAACCCCTGTCACGCGGACCTCACTGCGCAAGAGACAA 480
 C 508 GAUGUAUUAUAGAAUUGUUUUUCCUACGAAAGUGGGGCGAGAUUACUACGUGGAA 567
 L 481 GATGTGATCATGGAAGTTGTTTCCCAATGAAGTGGAGCCAGAAATTTCTAATCGGAA 540
 QY 568 UCCCAUUAUAAACCAAGAGAAAAAGAAAGAACUUCAGAGUUGCAAAUUAUUAACCU 627
 DB 541 TCACAACTAACAAATACCAAGAAAAAGAAAGAAACCTTCAAGATGCAAAATTTGCCCC 600
 QY 628 UUAAGUGUGUGGCAUUGUUAAGAGAGAAACUUGCCGAAAAAGAGAUUUUCUCCGAGU 687
 DB 601 TTGATGTGATACATACATGCTTAAGAAAGAGATGTCGGAAGAAACAGATTTCTCCAGTG 660
 QY 688 GUGUGUGGAAACAAGCAGUGUGUACUUGAAAGUGUGUACUUGACUCAAAGAACUGG 747
 DB 661 GCTGGCGGAACAAGCAGTGTATCATTTGAAGTGTTCATCTGACTCAGGAAACATGCTGG 720
 QY 748 GAACAGAUUUAUUAUCCAGUGGAGAGAGAGUAGAAUUAUUGUUAUUAAGUUAUUA 807
 DB 721 GAACAAATGTAACACCCAGAGAGAGAGAAAGTTAGAAACATGATCAATGTTAAAT 780
 QY 808 AUAAGCAGCAGAGACAUUAGUAGAAAGACAGCAUUAUCCAGAGUUAUUAUUA 867
 DB 781 ATTCTCTCCCGGACATATGTAAGAAAGCAGCACTATTCAGAGATTCACATGACATCCCTG 840
 QY 868 UUGAGAUUGGCGACAGACACAGAUUGGCGGAGCAAGAGUUGUGACAUUUCUAGCAG 927

DB 841 CTGGAATATGCCACAGTACACAGATTTGGTAATAGATGTGAAGCATCTTAACAG 900
 QY 928 AACCACAGAGAGAGACAGCGUGGAAUUAUUGCAAGGCTUCGAUUGGACUGAGAUACG 987
 DB 901 AATCCAAAGAGAGAAACAAGCTGTGATATATGCAAAACAGACAAATGGGTTAAGAAATAGC 960
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 QY 1108 GAGGAGUUCACAUUGUGUGGAAAAAGGCGCAACAGCUUUAUUAUUAUUAUUAUUA 1167
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 QY 1168 UUGAUUACGCUUAGUUGAGUAGAGAGAGAAACAGUACUAGUAGUAGAAUUAUUG 1227
 DB 1141 TTGATTCAAATTGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
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 DB 1201 GCGATGTGTTTC 1214

RESULT 15

US-09-506-286B-18
 ; Sequence 18, Application US/09506286B

; Patent No. 6482414

; GENERAL INFORMATION:

; APPLICANT: Dowling, Patricia W.

; APPLICANT: Youngner, Julius S.

; APPLICANT: The University of Pittsburgh, of the Commonwealth

; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

; FILE REFERENCE: EO-1-C2

; CURRENT APPLICATION NUMBER: US/09/506, 286B

; PRIOR APPLICATION NUMBER: 2000-02-16

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: PCT/US99/18563

; PRIOR FILING DATE: 1999-08-12

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 18

; LENGTH: 1214

; TYPE: DNA

; ORGANISM: Equine influenza virus H3N8

US-09-506-286B-18

Query Match 40.1%; Score 938.8; DB 4; Length 1214;
 Best Local Similarity 68.0%; Pred. No. 1.4e-279;
 Matches 825; Conservative 217; Mismatches 172; Indels 0; Gaps 0;

QY 28 AUGGAAAGAAUAAAAGAAUUAUUGGAGUUGGCGACUCGCGAGAUACUA 87
 DB 1 ATGGAGAGATTAAGAAAGATGAGAGATCTAATGTCACAAATCCGACCGGAGATCTA 60
 QY 88 AAAAAACGACAGUGGACCAUUGGCGCAUUAUUAGAAGUACAUCAGGAGGAGAGAA 147
 DB 61 AAAAAAATACTGTGGACCAATGCGCATATCAAGAAATACATCAGGAAAGACAGAG 120
 QY 148 AAGAACCCGUCACUUGAGUAGAAUUGGAGUAGGCAUUGAAUUAUUAUUAUUAUUA 207
 DB 121 AAGAACCCGCGACTTAAGATGAAGTGAATGATGCGCAATGAATATCCCAATTAACAGAGAT 180
 QY 208 AAGAGAAUAAACAGAAUUAUUGUUGGAGAAUUGAGAAAGGCGCAAAUUAUUGGAGUAAA 267
 DB 181 AAGAGATTAATGAATATGATCTCTGAGAGAAATGAACAGGCGCAAAACCTTTGGAGCAAA 240
 QY 268 AUGAGAUUGGCGGAGUUGGAGUUGUAGUAGUUAUUAUUAUUAUUAUUAUUAUUA 327

Db 241 ACGAAGATGCTGGCTCAGACCGCGTAATGTATCACTCTGGCAGTGCATGTGGAT 300
Qy 328 AGAAUUGACCAUGACAAGUACGUGUUAUCCAAAUAUCUUAUUUUGAG 387
Db 301 AGGAATGACCAACAGACCAATTCATTCAGAAAAGTCACAAAACCTAATTTGAA 360
Qy 388 AAAAGUCAAAGUUAAAACUGGAACUUGGCCUUCUUAUUUAGAAACCAAGUCAA 447
Db 361 AAAAGTGAAGATTAAACCGAACCTTGGCCCGTTCATTTAGAGATCAAGTCAAG 420
Qy 448 AUAAGCCGAAGUUGACUAAAUCUGGUCAUGCAGACUACUGUCCAAAGGAGCAG 507
Db 421 ATAAAGCGAAGATTATGTAACTTGATACGCGAGCTCAGTGCCTAAGAGACACAA 480
Qy 508 GAUUGUAUUGAUGAAGUUGUUUCCUUAAGAAUGGCGGCCAGAUACUAAUGCGAA 567
Db 481 GATGTGATCATGGAAGTTGTTTCCCAATGAAGTGGAGCCAGAAATTCMAATCGAA 540
Qy 568 UGCAGAUUUAACAUAACCAAGAGAAAAGAAAGAACTUCACAGAUUGCAAAAUUUCAC 627
Db 541 TCACAACTAACTAATACCAAGAGAAAAGAAAGAACTTCAGAGCTGCAGAAATGCCCC 600
Qy 628 UUGAUGUUGCGUACAUUGUAGAGAGAACTUUGUCCGAAAACGAGAUUUCUCCAGU 687
Db 601 TTGATGTAGCAATACCTAGTAAGAGAGGTTGGTCCAGAAAACAGATTCCTCCAGTG 660
Qy 688 GCUUGUGAACAAGCAGUGUGUACAUGAAGUGUUGACUUGACUACAAGAAACUUGCUG 747
Db 661 GCTGGCGGAACAAGACGTATATACATTTGAAGTTGTGATCTGACAGGAACATGCTGG 720
Qy 748 GAACAGAUUUAACUUCAGUGUGAGAGAAUGAGAAUUGAUGUUAUCAAAGUCAAU 807
Db 721 GAACAAATGTACACCCACGAGAGAGAAAGTTAGAAACGATGACATGATCAAAAGTTAAT 780
Qy 808 AUVGAGCCAGAGCAUUGUAGAGAGAGAGAUUACAGAUUACUUGCAUUCUUA 867
Db 781 ATTGCTGCCCGGACATGTGTGAAGAGGACAGATATCAGCAGATCCATGCAATCCCTG 840
Qy 868 UUGGAGUUGCCACAGACAGACAGAUUGCGGAGCAAGAGUUGGACAUUCUUAAGCAG 927
Db 841 CTGGAATGTGCAACAGTACAGATGTGTGAATTAAGATGTAGACATCTTAAGCAG 900
Qy 928 AACCCACAAGAGACCAAGCUGUGAAAUUAGCAAGCUGCAUUGGACUAGAGAUACG 987
Db 901 AATCCACAGAGAGAACAGCTGTGATATATSCAAACGACAGCAATGGGTTAAAGATTAG 960
Qy 988 UCAUUCUUCAGUUUGCGGUGUACAUAUUUAGAACAGCGGACUACUAGUCACAGAGA 1047
Db 961 TCATCATTCAGCTTGTGTGATTCACCTTAAAGAACAGTGTATCATCAGTCAAGAGA 1020
Qy 1048 GAGGAAGAAGUCUUAACGGGCAUUCUUAACAUUGAUAUUAAGGUGCAGAGGAAUAC 1107
Db 1021 GAAGAAAGAAATCTTAACGGGCACTTCAACATTTGAAATTAAGTGCATGAAGGCTAT 1080
Qy 1108 GAGGAGUUCACAUGGUGGAAAAGGCAACAGCUUAUCUAGAAAGCAACAGAGAGA 1167
Db 1081 GAAGAAATTCACAAATGTCGAAAGAGAGCAACAGCATTTCTAGAAAGCAACAGAGA 1140
Qy 1168 UUGAUCAGCUCUAGUUGAGUAGAGACGAAACAGUGCAUAGCUGAAAGCAUAUUGUG 1227
Db 1141 TTGATTCATTCATGTAGTAGTGAGAGATGAAACATCAATTCGTGAAGCAATATTGTA 1200
Qy 1228 GCCAUGGUUUUUC 1241
Db 1201 GCCATGTGTTTC 1214

QY 121 AAGAAUACACUACGAGGAGCGAGAAAGAAAGCCGCGUACUUGAGUAGAAUUGAGUAG 180
 DB 121 AAGAAATACATCAGAGAAAGCAAGAGAAAGAAAGCCCGCACTTAGATGATGAGATGATG 180
 QY 181 GCAATGAATUUUCCGAAUUAACGCGGCAAGAGAGAAUACAGAAUAGAUUUCUGAGAGAAU 240
 DB 181 GCAATGAATATCCCAATTTACAGCAAGATTAAGAGAAATTAAGAAATTAATTCCTGAGAGAAAT 240
 QY 241 GAGCAAGGCGCAAAACUUCUUGAGUAGUAGAAUUGAGUAGUAGCGAGUAGCGAUUCGUGUAGUA 300
 DB 241 GAGCAAGGCGCAAAACCTTTGAGAGAAAGAGAAAGATGCTGCGTCAAGACCGGCTAATGTA 300
 QY 301 UCAACUUCUGUGUAGUAGUAGUAGAAUUGAGAAUUGAGAAUUGAGAAUUGAGAAUUGAG 360
 DB 301 TCACCTCTGCGAGTGAATGAGTGAATGAGAAATGAGAAUUGAGAAUUGAGAAUUGAGAAUUGAG 360
 QY 361 CCAAAAUUCUACAAACUUAUUUUGAGAAUUGAGAAUUGAGAAUUGAGAAUUGAGAAUUGAG 420
 DB 361 CCAAAAGTCTACAAATCTTATTTTGAAGAAATTTGAAGAAATTTGAAGAAATTTGAGAAATTTG 420
 QY 421 CCUGUACUUUUUGAGAAACCAAGUCAAUUAACGCGAGAGUAGUAGUAGUAGUAGUAGUAGUAG 480
 DB 421 CCCGTTCACTTTTGAAGATCAAGTCAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 481 GCAAGACUUCAGUGCCAGAGAGGACAGAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 540
 DB 481 GCGGACCTCAGTGCCAAAGAGACCAAGATGTGATATGAGAAAGTTGTTTCCCAAAATGAA 540
 QY 541 GUGGAGGCGCGAGAUACUUAACUUCGAGAUUCGCAUUAACUUAACUUAACUUAACUUAACUUA 600
 DB 541 GTGGAGGCGCGAATTTCTAAACATCGGAATCAACAACTAACATTAACAAAGAGAGAAAGAA 600
 QY 601 GAAACUCCAGAUUUGAAAAUUCACCUUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 660
 DB 601 GAACTTCAGAGCTGCAAAATTTGCCCTTGATGATGATGATGATGATGATGATGATGATGATG 660
 QY 661 GUCGCGAAAAACGAGAUUUCUCCAGUUGUGUGUAGAAACAGAGUUGUAGUAGUAGUAGUAGUAG 720
 DB 661 GTCCGAAAAACAAAGATTTCTCCCAATGCTGCGGAGAAACAGAGATGTATTAATTTGAAATG 720
 QY 721 UUGGACUUGACUUAAGAAACAGUUCGAGAAACAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 780
 DB 721 TTGCACTCTGATCTCAGAGAGAAACATGCTGAGAAATGTACACCCGAGAGAGAAATTTGA 780
 QY 781 AAUGAUAGUUGUAGUACAAAGUUAUUUUGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 DB 781 AACGAT 840
 QY 841 GUUAGCAGAGUACUACUAGCAUUCUUAUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 900
 DB 841 GTATCAGCAGATCCACTAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 QY 901 ACAAGAGUUGUAGAUUCUUAUUGAGAGAAACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 DB 901 ATTAAGAGATGTAGATCTTAAAGCAATTCACAAAGAGAGAAACAGCTGTGATTAATGAC 960
 QY 961 AAGGUGCAUUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1020
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 QY 1021 AGAAGCAGCGAGUACUAGUCAAAG 1080
 DB 1021 AGAAGCAGCGAGATCAATCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 QY 1081 UUGAAAAUAGGUGUAGUAG 1140
 DB 1081 TTGAAAAATAGAGTCAATGAGTCAATGAGAAATTTCAACAATGCTGAGAAAGAGAGAGAGAG 1140
 QY 1141 GCUUUAUUCAGAGAAAGCAACGAGAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1200
 DB 1141 GCAATTTCTAGAGAGAGAGAGAGAGAGATTTGATTAATGATTAATGATTAATGATTAATGATTA 1200

QY 1201 CAGUCCAGUAGCUGAGCAUUAUUGUGGCGCAUGUUAUUUUCACAGAAAGAUUGUAGUA 1260
 DB 1201 CAATCAATTCCTAGACCAATTAATTTAGCATGATGATTTTCGCAAGAAATGACAGAA 1260
 QY 1261 AAAGCAGUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1320
 DB 1261 AAAGCAGUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1320
 QY 1321 CAUCAAUUUUUAGCAUUUUUAG 1380
 DB 1321 CATCAATCTTGAAGGAGATTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 QY 1381 GAAACAUUUCAGCAUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1440
 DB 1381 GAAACCAATCCAGCAATGTGATGAGAAATGAGAAATTTGCTGCAATGAGAGAGAGAGAGAG 1440
 QY 1441 GAGUUGUAGUAG 1500
 DB 1441 GAGATGATCAATTTGAG 1500
 QY 1501 GAGAGAGUAGUAGUAG 1560
 DB 1501 GAG 1560
 QY 1561 CUACUUAUUCUUGAG 1620
 DB 1561 CTACTGCTCCCTGAAG 1620
 QY 1621 UCAUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1680
 DB 1621 TCATCAATCAATTAATGAG 1680
 QY 1681 UGAGAUACUAGAGAAACUGGAGAAACUGUUAUUUUGAGUAGUAGUAGUAGUAGUAGUAGUAG 1740
 DB 1681 TGAGATATCAAGAGAAATTTGGAGAAATTTGAGAAATTTCAATGATGATGATGATGATGATGAT 1740
 QY 1741 UACAUUAUUUUGAGAUUUGAG 1800
 DB 1741 TACAAATTAAGATTAATTTGAG 1800
 QY 1801 UACAGUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1860
 DB 1801 TACAGCGGTTTGTGAAG 1860
 QY 1861 ACCAGCCAGAUUAUUUUAUUUUAUUUUAUUUUAUUUUAUUUUAUUUUAUUUUAUUUUAUUUUA 1920
 DB 1861 ACAGCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
 QY 1921 CAGUUCUUCUACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1980
 DB 1921 CAGTTCTCTTCTTGAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 1980
 QY 1981 AAUUUCUUAUUUUAUUUUAUUUUAUUUUAUUUUAUUUUAUUUUAUUUUAUUUUAUUUUAUUU 2040
 DB 1981 AATTTCCCAAGTGTCAATCAATTAATTAAGCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
 QY 2041 GCUAGCAGUUAUUCUAG 2100
 DB 2041 GAGAGTCCGCTTACTGAAG 2100
 QY 2101 AGAGAGUUCUACUUGGCGCAAG 2160
 DB 2101 AGAGAGTTCCTCAATTTTGAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
 QY 2161 GAACTGAGCAAACTTTGCAAG 2220
 DB 2161 GAACTGAGCAAACTTTGCAAG 2220
 QY 2221 GUGUUGUUAUUGAG 2280
 DB 2221 GTGTTGATTAATGAAG 2280
 QY 2281 AAAAGAGUUCGAGUAGGCAUCAAUUAUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 2340

Db 2201 AAAAGGATTCGGATGCCCATCAATTAGTGTGATTTGTTTAAAAACGACCTGTTTCTAC 2340

Qy 2341 U 2341

Dd 2341 T 2341

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RESULT 2
US-10-065-133A-47
: Sequence 47, Application US/10065133A
: Publication No. US20030199074A1
: GENERAL INFORMATION:
: APPLICANT: Dowling, Patricia W.
: APPLICANT: Youngner, Julius S.
: TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSSES
: FILE REFERENCE: BG-1-C2-1
: CURRENT APPLICATION NUMBER: US/10/065,133A
: CURRENT FILING DATE: 2002-12-10
: PRIOR APPLICATION NUMBER: PCT/US99/18583
: PRIOR FILING DATE: 1999-08-12
: PRIOR APPLICATION NUMBER: 09/133,921
: PRIOR FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 108
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 47
: LENGTH: 2341
: TYPE: DNA
: ORGANISM: Equine influenza virus H3N8
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (28)..(2304)
: OTHER INFORMATION:
: US-10-065-133A-47

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Query Match	77.0%	Score	1801.8	DB	13	Length	2341	
Best Local Similarity	66.1%	Pred.	NO.0					
Matches 1547	Conservative	457	Mismatches	337	Indels	0	Gaps	0

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Db	1 AGCAAAAGCGAGGTCAATATATTCAATTATGGAGAGATTTAAAGAACTAAGAGATCTTAATG	60
OY	UCCGAGUCUGGCACUUGCCGAGAUACUACAATAAACCAKAGUGACCAUAUGGCCUAUAU	120
Db	61 TCACAATCCCAGCACCCGCGAGATACTCAACAAAACTACGTGGACACATGGCCCATATTC	120
OY	AACAGUACACATCAGAGGACGAGAAAGAACCCGUCACUWAGGAGUAAUAGSUAGUAG	180
Db	121 AAGAAATATCACATCAGAGAAAGACAAGAGAAAGAACCCGCACTTAAAGATTAAGTGGATGATG	180
OY	GCAUAGAAAUUAVUCGUAUACAGCCGCAAGAGAGUAACAGAAAUAGUAVUCUGAGAGAAU	240
Db	181 GCAATGAATATCCCAATTATCAGCAGATTAAGAGATTAATGAAATGATTCCTGAGAGAAAT	240
OY	GACCAAGGCGCAACUCUAUGAGUAAAUAGAGUAGCCGAGUCCGUGAGUAGUGUA	3000
Db	241 GAACAGGGGCAAAACCTTTGGAGCAAAAAGAACGATGCTGGCTCAGACCGGCTAATGTGA	3000
OY	UACACUUCUGUCUUGACUUGUGGAAUAGAAUUGSACCAGUACAAGUCGUTUCAUUAU	360
Db	301 TCACCTCTGGCACTGTGCATGTGGAAATAGAAATGGAACAAACGAGACCAATTCATTAT	360
OY	CCAAAAAUUCACAAAACUUAUUUUGAGAAUGCAAAAGUUAAAAACUAGAACCUUUGGC	420
Db	361 CCAAAAGTCCACAAAACCTTATTTTGAAAAAGTTGAAAGATTAAACACGSAACCTTTGGC	420
OY	CCUGUCCAUUUNAGAAACCAAGUCAAAUAAGSCGAGAGUGUACAUAUAVUCUGGUCAU	480
Db	421 CCCGTTCAATTTTAGAATCAAGTCAAAAGATTAAGACGGAATGTTGTATGAACCTCGTCAAC	480
OY	GCAGACUUCAGUCCCAAGAGCACAGUUGUAUCAUGAAUGUUUUUUCCUAAGGA	540

Db	481	GGCGACCTCAGTGGCCAAAGAGCAACAAGATGTGATCATGTGAAGTTGTTTCCCAATATGA	540
QY	541	GUGGGGGCTCAGAGAUACAAGCCGUAUUGCGAAUUGCAUUAACAUAACCAAGAGAAAAAGAA	600
Db	541	GTGGGAGCGCAAAATTCTTAACATCGGAATCAACAATTCAATTAACCAAGAGAAAAAGAA	600
QY	601	GAACTUCACGAGUUGGAAAAUUTUACCTUUUGAUUGUUGGUUUAUUGUUAAGAGAGAAACUU	660
Db	601	GAACTTCACGAGCTGCAAAAATTGCCCCCTTGTATGTGATCATCATGTGAAGAAAGATTTG	660
QY	661	GUCCGAAAAAGAGAUUUUUCUCCAGUUGUCUGUGGAAACAACAAGUGUUAUAUUGAGUG	720
Db	661	GTCCGAAAAACAAGTTCTCTCCAGTGGCTGGCGGAACAACAAGTGTATATCACTTGAATGG	720
QY	721	UUGCACTUUGACUCUCAAAGAACUUGCGGAAACAGAUUUAACUCCACAGUGGAGAAAGUGAGG	780
Db	721	TTTGCACTCGACTCAGGGGAACATGCTGGGAACAAATTGTACCCCGAGAGAGAAAGTTAGA	780
QY	781	AUUGAUUGUUGUUAUACAAGUUAUUAUUGCAGCCAGACCAUUGUUAAGAAAGACACA	840
Db	781	AACAGATGCAATTGATCAAAAGTTTAATTAATGCTGCCCGGAACATATGTAGAAGAACGACA	840
QY	841	GUUACAGAGAUUCCAUAUUGCAUUCUUUAUUGAGAUUGUGCCAACAGACAACAUAUUGCGGG	900
Db	841	GTATTCAGCAAGATCCACTGTCAATCCCTGCTGGAATGTGCAACATGATCAAGATTTGTGTA	900
QY	901	ACAAGAUUGUGGACAUUUCUUAUGGACAGAACCCACAACAAGAGCAACGUCUGGAAAUUAGC	960
Db	901	ATAAGATGTGTAGACATCTCTTAAGCAAGAAATCCAACAAGAGAAACAAGCTGTGGAATTATGC	960
QY	961	AAGCTUGCAUUGGACUAGAGAUACAUCUACAUCUUAUUGGCGGGUUUUCACAUUUAAG	1020
Db	961	AAACACAGCAAGGAGGTATTAAGAAATTAGCTCATCATTCAGCTTTGGATTCACCTTTAAG	1020
QY	1021	AGAAACAAGCCGAGUACUACGUCACAGAGAGAGAAAGAAAGUGUCUUAACGGCAUUCUCAAACA	1080
Db	1021	AGAAACAAGTGAATCATCACTCAAGAGAGAGAAAGAAAGTCTTACGGCGCACTTCAACA	1080
QY	1081	UUGAAAAUUAAGGUGCAUUGAGAGAGAGAACGAGAGUUCACAUUGUGUGGAAAAAGGCAACA	1140
Db	1081	TTGAAAAATTAGAGTGCATGAAGGCTATGAAGAAATTCAACAATGTGTGGAAAGAGCAACA	1140
QY	1141	GCUUAUUCUAGAAAAGCAACCAAGAGAUUGUAUUCAGCGUAUUGUAGUGGAAAGAGCAAA	1200
Db	1141	GCCTATTCTCAGAAAAGGCACCAAGAAAGATTGCTCAATTGATATGTAAGGAGAGAGATATA	1200
QY	1201	CAGUCGUAUGCUGAGAUUAUUGUGGCCAUUGGUUAUUCACAAGAAAGAUUGUUAUGUA	1260
Db	1201	CAATCCAAATTGCTGAAGCAATATATTGTAGCCATGTGTGTTTCGCAAGAAAGATTGCAATGA	1260
QY	1261	AAAGCAGUUAAGGUGUAUUCUGAAUUTUGGUUAUUGAGGCAAAUUCACGCAUUGUAUUCCCAAG	1320
Db	1261	CAACGATGTGAGGCGAATTTGAACCTTCTTAATAGAGCAAAATCAACGCTTGAACCCCATG	1320
QY	1321	CAUCCACUUUTUAGACAUUUTUCAGAGAGUCCGAAAGUUCUUUUCAAAUAUUGGGGAAUUT	1380
Db	1321	CATCAACTCTTGAAGGCAATTTCCAAAAGATGCCAAAAGTGCCTTTTCACAAATTTGGGGGATTT	1380
QY	1381	GAAACAUUUCGACAUUGUGGGAUUGAUUUGGGGUUAUUAACAAGCAUACUCCACAAACACA	1440
Db	1381	GAACCCCATTCGACAAATGTGATGTGGGAATATGTGAATTATTTGCTTGACATGACCCCAAGCAAC	1440
QY	1441	GAGAUUGUCAAUAGAGGGGUUAAGAGUACGCAAAAUUGGGCGUAGUAUUAUUCUCCAGCGCG	1500
Db	1441	GAGATGTCTATTGAAGAGAGTGAAGATCAGCAAAATGCGAAGTGTAGATACTCCAGCACT	1500
QY	1501	GAGAGAGUAGUGUAGACAUUGACCCGCUUUTUUGAGAGUUCGAGACCAACGAGAAAUUGUA	1560
Db	1501	GAGAGAGTGTGTGTGACCATTCAGCCGTTTTTTAAAGATTTCCGGGATTCAAAAGGGGCAACATA	1560
QY	1561	CUUAUUAUUCUUGAGAGAGUUAUGUUAUUAACAGGAAACAGAGAAACUAGCAUUAUUAUUAAC	1620
Db	1561	CTACTGTGTCCTTGAAAGAGTCAAGTGAACACAAAGAAAGGAAAGCTGTACATAATATTTAT	1620

[illegible][illegible]

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Db      961  TCAATCTTCAAGCTTTGGATTCACCTTTAAGAGAAACAGTGGATCATCATGCAAGAGAA 1020
Qy      1048  GAGAAAGAAAGUUCUUAACGCGCAUUCUUAACAUUAGAAUUAAGGUGUAGAGAGAUAC 1107
Db      1021  GAAGAAGAAATGCTTAACGGGCAACCTTCAAAACATTAATAAGATGATGAAGGCTAT 1080
Qy      1108  GAGAGAUUACAUAUGUUGUGAAAAGGCGAACGCTUUAUCUAGAAAGCAACGAGAGA 1167
Db      1081  GAAGAATTCACATATGATCGAGAGAGCAACAGCATTCCTCGAAGAGCAACGAGAGA 1140
Qy      1168  UUGAUACGUCUUGUUGUGAGAGAGCAACAGUCUAGUGUGAGCAUUAUUAUUGUG 1227
Db      1141  TTGATTCATTTGATGATGAGAGAGAGATGAACATATTCGAGACCAATTAATTGTA 1200
Qy      1228  GCCAUGUUAUUUUCACAGAGAAUUGUUAUUAAGAGUUAAGAGUAGUUCUGAAUUC 1287
Db      1201  GCCATGCTGTTTTCGAGAGAAAGATTGCATGATTAAGAGAGTTGAGGCACTTGAATTC 1260
Qy      1288  GUUAUUAAGGCAAAUACGCGAUUUAUCCCAUGCAUAACTUUUAAGACUUAUUCAGAG 1347
Db      1261  GTTAATAGAGCAAAATCAGCGCTTGAACCCCATGCAATCACTTGGAGCATTCGAAAA 1320
Qy      1348  GAUGGAGAAAGUGUUAUUAAGAAUUGGGAUUAUGAUCUAGAGUAGUUGGGAUUG 1407
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Qy      1408  AUUGGAGUUAUUAACAGACAUUACUCCAGACACAGAGAUUGCAUUAAGAGGAGUAGAG 1467
Db      1381  ATTGGAATTTGCTCTCAATGACATGACCCAGAGCAACGAGATGTCATTGAGAGAGTGAAGT 1440
Qy      1468  ACCAAAUUGGCGUAGUAGUUAUUCUCCAGCGCGAGAGAGUAGUGUGAGCAUUAACCG 1527
Db      1441  AGCAAAATGAGAGTGTAGTATGATCTCAGACATGAGAGAGATGATGATGAGATGAGACCGT 1500
Qy      1528  UUUUUGAGAGUUGUAGAACCAAGAGAAUUGUUAUCUUAUUCUUGAGAGAGUAGUGUA 1587
Db      1501  TTTTAAAGAGTTCGGGATCAAAAGGAGAAACATATCTCTCTCCCTGAGAAAGTCAAGTGA 1560
Qy      1588  ACACAGAGGAAACAGAGAAACUGACCAUUAUCUUAUCUUAUUGUUGGAGAGUUAU 1647
Db      1561  AACAAGAGAAACGAGAAAGCTGACATTAATTTATTCATCAATGATGATGAGAGATTAAT 1620
Qy      1648  GGCCCGUAGAGUUGUUGUUAUUAUACUUAUCAGUGAGUAGUAGUAGAAACUGGAGAA 1707
Db      1621  GGTCCGGAATCAGTGTTCATTAATCTATCAATGATGATGATGATGATGATGATGATG 1680
Qy      1708  AAAAUUUGAGUUGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1767
Db      1681  AAAATTCGAATGTCACAGAGATCCCAATGTTATTAATTAATTAATTAATTAATTAATTA 1740
Qy      1768  CAGUCUUAUUGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1827
Db      1741  CAGTCCCTGCTCTTACGAGGACACAGAGACCAATTAACGCGGTTTGTAAAGAACCTGTTT 1800
Qy      1828  CAACAAUUAUGAGAGUUAUCUUGAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1887
Db      1801  CAGCAAAATGCGAGATGTACTTGGAACATTTGATACGCTCAATTAATAATAAATCTCTCCT 1860
Qy      1888  UUUUGACCGCGCCCGCACAAAGCAAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1947
Db      1861  TTTTCCGCTGCTCTCTCCGAAACAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1920
Qy      1948  AGGAGUACAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2007
Db      1921  AAGAGATTCGAGATGAGATGATGTAAGAGAGATTTCCCACTGTTCACTAATCAATTA 1980
Qy      2008  ACCACUUAAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2067
Db      1981  GCACTTAAGAGAGGCTCACTCTCCGAAAGAGATGAGAGGCTGCTTAAGTAAGACCAAGT 2040
Qy      2068  GAAGCACAUCUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 2127

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Db      2041  GAAGTACGCGTGGAGATGAATCTGCTGTTCTAAGAGGTTTCTATTATTAAGTAAGAA 2100
Qy      2128  GAUUGAGAUUUGAGACGACAUUUAAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2187
Db      2101  AAGAAGAGATATGAGCCGACGACTAAGCATCAATGAATGAGCAAACTTGGAAAAAGGAG 2160
Qy      2188  AAGCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2247
Db      2161  AAAGCTAATGCTAATTTTGGGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Qy      2248  UCUGACAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2304
Db      2221  TTAAGCTACTTACTTACTGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2277

RESULT 4
US-10-065-133A-49
; Sequence: 49; Application: US/10065133A
; Publication No.: US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 49
; LENGTH: 2277
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-49

Query Match      74.5%; Score 1744.2; DB 13; Length 2277;
Best Local Similarity 66.2%; Pred. No. 0;
Matches 1508; Conservative 436; Mismatches 333; Indels 0; Gaps 0;

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Db      1  ATGAGAGAAATTAAGAAAGTGAAGATCTAATGTCACAAATCCGCAACCCGAGATTA 60
Qy      88  ACAAACCCACAGUGGACCAUUAUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 147
Db      61  ACAAAACCTACTGTGACACATGGCCATTAATCAAGAAATACATCAAGAGACAAAGAG 120
Qy      148  AAGAACCAGCAUUAUGAUGAAUUAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGA 207
Db      121  AAGAACCAGCAUUAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUG 180
Qy      208  AAGAAGUUAACAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 267
Db      181  AAGAAGUUAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 240
Qy      268  AUGAGUAGUCCGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 327
Db      241  ACGAAGCATGTGCTGACAGACCGGTAATGTATCACTCTGGGAGATGATGATGATGAT 300
Qy      328  AGAAUAGACCAUUAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUG 387
Db      301  AGAATGAGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy      388  AAGAGUCAAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 447
Db      361  AAGCTTAAGAAATTAAGAAACAGAACTTTGGCCCGCTTCAATTTAAGAAATCAAGT 420
Qy      448  AUAAGCCGAAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 507
Db      421  ATAAGACGAGAGATTTGATGTAATCAACCTGTGTCAGCGGAGACCTCAAGTCCAAAG 480

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QY 361 CCAAAAUUCUACAAACUUAUUGAGAAAGUCGAAAGGUAUAAACUUGAACCUUUGGC 420
Db 361 CCAAAAUUCUACAAACUUAUUGAGAAAGUCGAAAGGUAUAAACUUGAACCUUUGGC 420
QY 421 CCUUGCCAUUUUUGAAGCAAGUCAAUUAUAGCCGAAAGAGUUGACUAUAAUUCUGUACU 480
Db 421 CCUUGCCAUUUUUGAAGCAAGUCAAUUAUAGCCGAAAGAGUUGACUAUAAUUCUGUACU 480
QY 421 CCGGTCATTTTAAAGATCAAGTCAAGATTAAGACGAAAGTGAAGTGAACCCGTGTCAC 480
Db 421 CCGGTCATTTTAAAGATCAAGTCAAGATTAAGACGAAAGTGAAGTGAACCCGTGTCAC 480
QY 481 GCAGACUUCAGUGCCAGAGAGGACAGAGUUGAUCAGAGAGUUGUUGUUGCCUUAACGAA 540
Db 481 GCAGACUUCAGUGCCAGAGAGGACAGAGUUGAUCAGAGAGUUGUUGUUGCCUUAACGAA 540
QY 481 GCGACCTCAGTGCAGAAAGAGACAGAGATGTGATCAGAGAGTGTTCCTCAATGAA 540
Db 481 GCGACCTCAGTGCAGAAAGAGACAGAGATGTGATCAGAGAGTGTTCCTCAATGAA 540
QY 541 GUGGGGCGCAGAGUAUCUACGUGCGAAGUUGCAUUAACUUAACCAAGAGAGAGAGAA 600
Db 541 GUGGGGCGCAGAGUAUCUACGUGCGAAGUUGCAUUAACUUAACCAAGAGAGAGAGAA 600
QY 541 GTGGAGGCGAGAAATCTAAACATCGGAATCAACAACTAAATPACCAAGAGAGAGAGAA 600
Db 541 GTGGAGGCGAGAAATCTAAACATCGGAATCAACAACTAAATPACCAAGAGAGAGAGAA 600
QY 601 GAACUUCAGAGUUGCAAAUUAUUCACUUAUUGAGUUGGUAUUGUUGAGAGAGAACTU 660
Db 601 GAACUUCAGAGUUGCAAAUUAUUCACUUAUUGAGUUGGUAUUGUUGAGAGAGAACTU 660
QY 601 GAACUUCAGAGUUGCAAAUUAUUCACUUAUUGAGUUGGUAUUGUUGAGAGAGAACTU 660
Db 601 GAACUUCAGAGUUGCAAAUUAUUCACUUAUUGAGUUGGUAUUGUUGAGAGAGAACTU 660
QY 661 GUCCGAAAAAGAGAUUUCUCCAGUUGCUGUGGAGAGACAGAGUUGUACUUAUUGAG 720
Db 661 GUCCGAAAAAGAGAUUUCUCCAGUUGCUGUGGAGAGACAGAGUUGUACUUAUUGAG 720
QY 661 GTCCGAAAAAGAGAUUUCUCCAGUUGCUGUGGAGAGACAGAGUUGUACUUAUUGAG 720
Db 661 GTCCGAAAAAGAGAUUUCUCCAGUUGCUGUGGAGAGACAGAGUUGUACUUAUUGAG 720
QY 721 UUGCAGUUGACUUCAGAGAAACUUGCUGGAGACAGAGUUAACUUCAGUGGAGAGAG 780
Db 721 UUGCAGUUGACUUCAGAGAAACUUGCUGGAGACAGAGUUAACUUCAGUGGAGAGAG 780
QY 721 TTGCATCTGACTCAGAGGAAACATGCTGGGAAACAAATGTACACCCGAGAGAGAGTTA 780
Db 721 TTGCATCTGACTCAGAGGAAACATGCTGGGAAACAAATGTACACCCGAGAGAGAGTTA 780
QY 781 AAUGUUGUUGUUGAUAAGUUAUUAUUGCAGAGAGAGAGAGUUGAGAGAGAGAGAG 840
Db 781 AAUGUUGUUGUUGAUAAGUUAUUAUUGCAGAGAGAGAGAGUUGAGAGAGAGAGAG 840
QY 781 AAUGUUGUUGUUGAUAAGUUAUUAUUGCAGAGAGAGAGAGUUGAGAGAGAGAGAG 840
Db 781 AAUGUUGUUGUUGAUAAGUUAUUAUUGCAGAGAGAGAGAGUUGAGAGAGAGAGAG 840
QY 841 GUUAUCAGAGAUUCACUAGCAUUCUUAUUGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 GUUAUCAGAGAUUCACUAGCAUUCUUAUUGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 841 GTATAGAGAGAGATCCAGTACAGATCCCTGCTGGAGAAATGTCCAGAGAGAGAGAG 900
Db 841 GTATAGAGAGAGATCCAGTACAGATCCCTGCTGGAGAAATGTCCAGAGAGAGAGAG 900
QY 901 ACAAGAGUUGAGAGAUUCUUAUUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 ACAAGAGUUGAGAGAUUCUUAUUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 901 AATAAGAGATGTAGATCATCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 AATAAGAGATGTAGATCATCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 AAGGUGAGAUUGGAGACUAGAGUUCAGUUCUUAUUGAGAGAGAGAGAGAGAGAG 1020
Db 961 AAGGUGAGAUUGGAGACUAGAGUUCAGUUCUUAUUGAGAGAGAGAGAGAGAGAG 1020
QY 961 AAGGUGAGAUUGGAGACUAGAGUUCAGUUCUUAUUGAGAGAGAGAGAGAGAGAG 1020
Db 961 AAGGUGAGAUUGGAGACUAGAGUUCAGUUCUUAUUGAGAGAGAGAGAGAGAGAG 1020
QY 1021 AGAAGAGCGAGAUUCAGUUCAGUUCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1021 AGAAGAGCGAGAUUCAGUUCAGUUCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1021 AGAAGAGCGAGAUUCAGUUCAGUUCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1021 AGAAGAGCGAGAUUCAGUUCAGUUCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 UUGAAAUUAAGGAGUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 UUGAAAUUAAGGAGUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1081 TTGAAATAATAGAGTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 TTGAAATAATAGAGTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1141 GCUNUACUACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1141 GCUNUACUACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1141 GCUNUACUACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1141 GCUNUACUACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 CAGUGAGAUUGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db 1201 CAGUGAGAUUGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1201 CAGUGAGAUUGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db 1201 CAGUGAGAUUGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260

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RESULT 7
US-10-065-133A-22

; Sequence 22, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EO-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10

```

; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1232
; ORGANISM: Equine influenza virus H3N8
; US-10-065-133A-22

Query Match      40.2%   Score 941.4: DB 13; Length 1232;
Best Local Similarity 64.1%   Pred. No. 7.2e-262;
Matches 789; Conservative 261; Mismatches 181; Indels 0; Gaps 0;

QY 1111 GAGUUCACAAUGGUGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1170
Db 2 GAATTCACAAATGATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 61
QY 1171 AUUCAGUUGAUUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
Db 62 ATTCAATTGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
QY 1231 AUUGUAUUUUUUCACAAAGAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1290
Db 122 ATGCTGTTTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
QY 1291 AAUAGGCGAAAUUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1350
Db 182 AATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 241
QY 1351 GCGAAAGGCGUUUUUUCAAAUUUGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1410
Db 242 GCAAAAGTCTTTTCCAGAAATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
QY 1411 GGGGUAUUAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1470
Db 302 GAATATTTGCTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361
QY 1471 AAAAUGGGCGUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1530
Db 362 AAAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
QY 1531 UUGAGAGUUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1590
Db 422 TTAAAGATTTGGGATCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 481
QY 1591 CAGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1650
Db 482 CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541
QY 1651 CCUGAGUUGAGUUGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1710
Db 542 CCGGAAATGATGTTGGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 601
QY 1711 AUUCAGUUGUUCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1770
Db 602 ATTCAATTTGTCACAGAGATCCCAATGTTATTAATTAATTAATTAATTAATTAATTAAT 661
QY 1771 UCUGUUGUUCUUAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1830
Db 662 TCCCTGCTCTTGGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 721
QY 1831 CAAAUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1890
Db 722 CAATTCGAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
QY 1891 GCAAGCCGCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1950
Db 782 GCGGCTCTCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 841
QY 1951 GGAUCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2010

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Db      842  GGAATGGGAATGAGATTAATTGTAAGGCAATTCCTCCAGTGTCAATCAATTAAGCC 901
Qy      2011  ACUAAAGACUAAUUCUGGAAAGAGUGGCGACUUAACUAAAGACCGAGAUGA 2070
Db      902  ACTAAGAGGCTGCAAGTCTCTGGAAGAGATGCGCTTACTGAAGCCGAGATGA 961
Qy      2071  GGCACAUUCUGAGUGGAGUGCCUGUUCUGAGAGAUUCUUAUUCUGGCAAAAGAU 2130
Db      962  GGTACGGCTGAGATGATCTGTCTTAAGAGGGTTCATTTTAAGTAAAGAAAC 1021
Qy      2131  AGGAGAUAGACAGACGUAUAGAUCAUAGAUACUUGGAAAGAGAAAG 2190
Db      1022  AAGAGATATGGCCAGCACTAAGCATATGAATCTGACAAACCTTGCAAAAGAGAA 1081
Qy      2191  GCUAUAUACUAAUUGGCAAGAGAGACUGUGUGUAUUAAGAAACGAAACU 2250
Db      1082  GCTAATGTCTAATTTGGGCAAGGGAGCTGTGTGTAAATGAACGGAACCTGACTCT 1141
Qy      2251  AGCAUACUUAACUAGCAGCCAGACGACGCAAAAGAUUCGAGUGGCCAUUAUUG 2310
Db      1142  AGCACTACTTACTGACAGCCAGACGACGCAAAAGATTCGATGCGCATTAATGTGT 1201
Qy      2311  UGAUAUUGUUAUAAAGCAACCUUGUUCUACU 2341
Db      1202  TGAATGTTTAAAGCAACCTTGTCTACT 1232
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RESULT 8

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US-10-065-133A-19
; Sequence 19, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; TITLE OR INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EO-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1233
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(1196)
; OTHER INFORMATION:
US-10-065-133A-19
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Query Match      40.2%; Score 941.4; DB 13; Length 1233;
Best Local Similarity 64.1%; Pred. No. 7,2e-262;
Matches 789; Conservative 261; Mismatches 181; Indels 0; Gaps 0;
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Qy      1111  GAGUUCACAUAUGGUGGAAAAGGCAACGCUUAUCAGAAAGCAACACAGAGAUUG 1170
Db      3  GAATTCACATGTGCGAGAGAGCAACAGCCATCTCTCAGAAAGCAACAGAAATTTG 62
Qy      1171  AUUCAGCUGAUUUGGAGAGAGAGACAGUCGUAACUUAACGAATTAATTTGAGCC 1230
Db      63  ATTCAATTGTATGATGAGATGAGAGATGAACAATCAATTCCTAAGCAATTAATTTG 122
Qy      1231  AUGGUAUUTUACAAAGAAAGUUGUAUUAAGCAAGUUAAGAGUGUAUUCGUAUUC 1290
Db      123  ATGCTGTTTTCGCAAGAGATTCGATATAAAGCAATTCGAGCGCATTTTGAATCTCT 182
Qy      1291  AAUAGGCGCAAAUUCGCAUUGAUAUCCAUUGCAUUCUUAUUAAGCAUUTUUCGAA 1350
Db      1291  AAUAGGCGCAAAUUCGCAUUGAUAUCCAUUGCAUUCUUAUUAAGCAUUTUUCGAA
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Db      183  AATAGAGCAATACAGCGCTTGAAACCCCATGCATCACTCTTGAGGCAATTTCCAAAAGAT 242
Qy      1351  GCGAAAGUGUCUUTUUCAAUAUUGGGAAUUGAAUAUUCGACAAUUGUAUUGGAAUUG 1410
Db      243  GCAAAAGGCTTTTCCAGAAATTTGGGAGTTGAACCCATCGACAAATGTGATGGAAATG 302
Qy      1411  GGGGUAUUAACGACAGACUAGCTUCCAAAGCAGAGAGUUAUUAAGAGGGGUAAGAC 1470
Db      303  GGAATATTCCTCGACATGACCCCAAGCAGAGATGTCAATGAGAGGTGAGATCGAC 362
Qy      1471  AAAAUGGCGUGUAUUAUUAUCUAGCGCGGAGAGAGUAUUGUGAGCAUUGACCGG 1530
Db      363  AAAATGGAGTGAATGATGATCTCCAGCACTGAGAGAGTGTGTGATGATTAACCTTTT 422
Qy      1531  UUGAGAUUCGAGACCAACGAGAAAUUGUACUAUUCUUCGAGAGAGUACUGAAAA 1590
Db      423  TTAAAGTTTCGGGATCAAAAGGGAAACATTAATCTGTCCTCCGAAAGGTGAGTAAACA 482
Qy      1591  CAGGGAACAGAAACUGAACUAUAUCUAUCUACUUGCUGUAUUGUGGAGAUUAUUGCC 1650
Db      483  CAAGGAACGGAAGAACTGCAATTAATTAATTCATCATCATGATGTGGAGATTAAATGT 542
Qy      1651  CGUGAGUACUGUGUGUACUAUUCUAUUGAGUAUUCAGAAACUGGGAAACUGUUA 1710
Db      543  CCCGATCAATGTGTGTGATCAATCTTATCAATGATCATCGAACTGGAAATTTGAA 602
Qy      1711  AUUCAGUGUCUACUAUUCUUAUUGCUUAUAUAUUAUUAUUAUUGAGCCAUUUGAG 1770
Db      603  ATTCAATGTGTCACAGATTCACCAATGTTATACATTAATTAATTAATTTGAGCATTC 662
Qy      1771  UCUUAUUGUCUUAAGCCCAUUAUAGCCCAUAUACUGUGGUGUUGUAAGACUUAUUC 1830
Db      663  TCCCTGTGTCCTTGAAGGCGCAACCAAAACACCGGTTTGTAAAGAACCTGTGTTGAG 722
Qy      1831  CAAUAGAGGAGUUAUCUUGGGACAUUUGAUAUUCACCAAGAUUAUUAUUAUUAUUA 1890
Db      723  CAAATGCGAGATGATCTTGAACATTTATATCTGCTCAAAATTAATTAATTAATTA 782
Qy      1891  GCAGCGCGCCCAACCAAGAAUUAUUAUUGAGUUCUUCUUAUCUGACUGUUAUUGAG 1950
Db      783  GCGCGTGTCTCCCGGAAACAGATGATGACAGTTCTCTTTTGAATGATTAATGA 842
Qy      1951  GGAUACAGAAUAGAAUAUCUUGUAAGGGCAAUUCUUCUUAUUAUUAUUAUUAUUA 2010
Db      843  GGATCGGGAATGAGATCTTGTAAAGGCAATTCGCCAGTGTCAACTAATAATTAAGCC 902
Qy      2011  ACUAAAGACUAAUUAUUCUGGAAAGAGAUUCUGGCAUUAACUAGAACCCAAUUA 2070
Db      903  ACTAAGAGGCTTCACAGTCTCTCGAAAGATGCAAGTGTGCTTAAGAGACCCAGATGA 962
Qy      2071  GGCACAUUCUGAGUGGAGUGCGUGUUCUGAGAGAUUCUUAUUCUGGCGCAAGAA 2130
Db      963  GGTACGGCTGAGATGAAATCTCTGTCTTAAGAGGTTTCTATTTTAAAGTAAAGAA 1022
Qy      2131  AGGAGAUUUGACCGACGACUUAAGCAUUAUGAAUUGAGUUAACUUGGCAAGAGAA 2190
Db      1023  AAGAGATATGGCCAGCACTAAGCATTAATGAATGAACAACTTGCAAAAGGGAGAA 1082
Qy      2191  GCUAUAUUAUUAUUGGCGCAAGAGAGACUGUGUGUUAUUAAGAAACGAAACU 2250
Db      1083  GCTAATGTCTTAATTTGGGCAAGGGGACGTGTGTGTAAATGAACGGAACGTGACTCT 1142
Qy      2251  AGCAUUAUUAUUGAGCAGACGACGACGCAAAAGAUUUGGAGGCAUUAUUAUUG 2310
Db      1143  AGCATTAATCTTACTGACAGCGACGACGACGCAAAAGATTCGATGCGCATTAATGTGT 1202
Qy      2311  UGAUAUUGUUAUAAAGCAACCUUGUUCUACU 2341
Db      1203  TGAATGTTTAAAGCAACCTTGTCTACT 1233
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RESULT 9

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US-10-065-133A-15
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; Sequence 15, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; '0-065-133A-15

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Query Match      40.1%; Score 940.4; DB 13; Length 1214;
Best Local Similarity 68.0%; Pred. No. 1.4e-261;
Matches 825; Conservative 218; Mismatches 171; Indels 0; Gaps 0;

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QY 28 AUGGAAAGAUUAAAGAAACUACGAAUUCGAGUUCGCGACUCGCGAGAUACUA 87
DB 1 ATGGAGAAATATAAGAACTGAGAGATCTAATGTCAATCCCGACCCGAGATACTA 60
QY 88 ACAAACACACAGUGACCAUUGGCGCAUUAUUAAGAAAGUACAUUCAGCGAGAGAA 147
DB 61 ACAAACACACAGUGACCAUUGGCGCAUUAUUAAGAAAGUACAUUCAGCGAGAGAA 120
QY 148 AAGAACCCGUCACUAGAGAUAGAUAGUAGGCAUUAUUAUUAUUAUUAUUAU 207
DB 121 AAGAACCCGUCACUAGAGAUAGAUAGUAGGCAUUAUUAUUAUUAUUAUUAU 180
QY 208 AAGAGAUUACGAAAUUGAUUUCUGACGAAAUUAGCAAGGCGCAUUCUUAUGA 267
DB 181 AAGAGAUUACGAAAUUGAUUUCUGACGAAAUUAGCAAGGCGCAUUCUUAUGA 240
QY 268 AUGAGUAGUCCCGGAGUCCGAGUUGUAGUAGUACUUCUGCGUUGACUAGUGA 327
DB 241 ACGAAGATGCTGCTGACAGACCGCGTAATGTATCACTCTGCGACGTACATG 300
QY 328 AGAAUUGACCAUUAAGAAUUCGUGUACUUAUUAUUAUUAUUAUUAUUAUUA 387
DB 301 AGAATGACCAUUAAGAAUUCGUGUACUUAUUAUUAUUAUUAUUAUUAUUA 360
QY 368 AAGAGUAGUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 447
DB 361 AAGAGUAGUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 420
QY 448 AUAAGCCGAGAGUUGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 507
DB 421 AUAAGCCGAGAGUUGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 480
QY 508 GAUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 567
DB 481 GAUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 540
QY 568 UCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 627
DB 541 TCACAACTAATCAATTAACCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 600
QY 628 UUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 687
DB 601 TTGATGAGTACATCTAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 688 GCUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 747
DB 661 GCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

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QY 748 GAACAGAUUACUUCAGAGUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 807
DB 721 GAACAAATGTACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 808 AUGGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 867
DB 781 ATTCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 868 UUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 927
DB 841 CTGAAATGTGCGACAGTACAGATTTGAGAAATGAGATGGTATGATCTTAAG 900
QY 928 AACCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 987
DB 901 AATCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 988 UCAUCCUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1047
DB 961 TCATCATTTACGCTTTGATGATTTACCTTTAAGAGAGAGAGAGAGAGAGAG 1020
QY 1048 GAGAGAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1107
DB 1021 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1108 GAGAGUACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1167
DB 1081 GAGAGUACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1140
QY 1168 UUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1227
DB 1141 TTGATTTCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1200
QY 1228 GCCAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1241
DB 1201 GCCATGCTGTTTTC 1214

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RESULT 10
US-10-065-133A-18
; Sequence 18, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; US-10-065-133A-18

```

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Query Match      40.1%; Score 938.8; DB 13; Length 1214;
Best Local Similarity 68.0%; Pred. No. 4.1e-261;
Matches 825; Conservative 217; Mismatches 172; Indels 0; Gaps 0;

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QY 28 AUGGAAAGAUUAAAGAAACUACGAAUUCGAGUUCGCGACUCGCGAGAUACUA 87
DB 1 ATGGAGAAATATAAGAACTGAGAGATCTAATGTCAATCCCGACCCGAGATACTA 60
QY 88 ACAAACACACAGUGACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 147
DB 61 ACAAACACACAGUGACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 120
QY 148 AAGAACCCGUCACUAGAGAUAGAUAGUAGGCAUUAUUAUUAUUAUUAUUA 207

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Db      121  AAGAACCCCGCACTTGAAGATGAAGTGAATGATGAAATACCAATTAACAGAGAT 180
Qy      208  AAGAGAGAUACAGAAUUGAUUUCUGAGAGAAUUGAGCAAGGCAAAUCUUAUGAGUAAA 267
Db      181  AAGAGATTAATGAAATGATTCCTGAGAGAAATGAAACAGGGGAAACCTTTGGAGCAA 240
Qy      268  AUAUGAGAUUCCCGGAGUUGGUGUGAUUGUUAUCCUUGGUGUGUAGUUGUAAU 327
Db      241  ACCAAGATGCTGGCTCAGACCCGTAATGTAATCACTTCGACGTGCAATGCTGAT 300
Qy      328  AGAAUUGACCAUUGACAGUACGUUUAUUGCAAAUUAUUGCAAAUUAUUGUAG 387
Db      301  AGGAATGACCAACAAAGAGCAACATTCATTAACAAAGTCCAAACCTTAATTTGA 360
Qy      388  AAAAGUGAAAGUUAUUAUUGAAACCUUUGGCGUUGUCCAUUUUUAAGAAACCAAGUCAA 447
Db      361  AAGTTGAAAGATTAATAACCGGACCTTTGGCCCGTTCACTTTAAGAAATCAAGTCAAG 420
Qy      448  AUAACCCGGAAGAGUUGACUAAAUCCUGUUAUGACAGACCTUCAGUCCAGAGGACAG 507
Db      421  ATTAAGCGGAGAGTGTATGTAACCTCGTCAACGCGACCTCAGTGCCAAAGAACACAA 480
Qy      508  GAUGUAUUGACAGUUGUUAUUGCUAAAGAGGGGGCCAGAGUUAUUGUAGGAA 567
Db      481  GATGTATATGAGAGTGTATTTCCCAAAATGAAGTGGAGCAAGATTCATTAATTCGAA 540
Qy      568  UGCCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 627
Db      541  TCACAACATAATTAACAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 600
Qy      628  UUGAGUUGUUGGUAUUGUUAUUGAGAGAAACUUGUCCGAAAGAGAUUUUCCGAGU 687
Db      601  TTGATGTGTGATCACTATGCTAGAAAGAGAGTTGTCCGAAAGAAAGAAAGATCTCCCAAGT 660
Qy      688  GUGUGUUGAAACAAGAGUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUG 747
Db      661  GCTGGCGGAAACAAGAGTGTATTAATTAAGTGTGATCTGACCTCAGGAAACATGCTGG 720
Qy      748  GAACAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 807
Db      721  GAACAATTAATTAACCCCGAGAGAGAAAGTAAAGAAAGATGATTAATTAATTAATTT 780
Qy      808  AUAUGACCCGAGAGCAUUAUGAGAAAGAGAGAGUUAUUGCAUUGCAUUGCAUUGCAU 867
Db      781  ATTGCTGCGCCGGAACATAGTAGAAGAGAGAGATGATGACATCCATGACATCCCTG 840
Qy      868  UUGAGAUUUGCCACAGCAACAGAUUGGCGGAGCAAGAUUGUUGUUAUUGUUGGAG 927
Db      841  CTGGAATGTGTCACAGTACAGAGATGTGTGAATTAAGATGTGATGATCTTTAAGCAG 900
Qy      928  AACCCAAACAGAGAGAGCUGUUGAAAUUAUGCAAGCUGUUAUUGGAGCUGAGAUUGAGC 987
Db      901  AATCCAAACAGAGAGAGAGCTGTGATTAATTAACAAAGAGAGAGAGAGAGAGAGAGAG 960
Qy      988  UCAUUCUUAUGUUGGCGGAGUUAUUAUUGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1047
Db      961  TCATCATTCAGCTTTGTGATTTCACTTTAAGAAAGAGAGATGATCAATGATCAAGAG 1020
Qy      1048  GAGGAAGAAAGUUGCUUAAGGAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1107
Db      1021  GAAAGAAAGAAATCTTAACGGGCAACCTTCAACATTAAGAAATTAAGTGCATTAAGGCTAT 1080
Qy      1108  GAGGAGUUAUUAUUGUUGGAAAGAGGCAAGCAGUUAUUAUUGAGAAAGCAAGAGAG 1167
Db      1081  GAGGAATTCACATATGTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy      1168  UUGAUUUGAGUUGUUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1227
Db      1141  TTGATTCATTAATGATTAAGTGGAGAGATGAACATCAATTCCTGAGAGAGATTAATGTA 1200
Qy      1228  GCCAGUUAUUAUUG 1241

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Db      1201  GCCATGTGTTTTC 1214

RESULT 11
US-10-065-133A-23
; Sequence 23, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1232
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1195)
; OTHER INFORMATION:
US-10-065-133A-23

Query Match      40.1%; Score 938.2; DB 13; Length 1232;
Best Local Similarity 63.9%; Pred. No. 6,1e-261;
Matches 787; Conservative 261; Mismatches 183; Indels 0; Gaps 0;

Qy      1111  GAGUUCACAUUGUGGGAAGGCAAGCAAGCAGUUAUUGCAAGAAAGCAACAGAGAUUG 1170
Db      2      GAATTCACAAATGCTGGGAAAGAGCAAGCAAGCAATTCGAAAGGCAACAGAGAGATTG 61
Qy      1171  AUAUGAGUUAUUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
Db      62  ATTCAATTAATGATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
Qy      1231  AUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1290
Db      122  ATGTGTTTTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
Qy      1291  AAUUGGCAAAUUAUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1350
Db      182  AATAGAGCAAAATCAGCCCTTGAACCCCATGCACTCACTTGAAGGCAATTCGAAAGAGAT 241
Qy      1351  GCGAAAGUGGCUUUAUUAUUGGGGAAUUGAACAUAUUGCAUUGAGAGAGAGAGAGAGAG 1410
Db      242  GCAAATATGCTTTTCCAGAAATTAAGGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 301
Qy      1411  GGGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1470
Db      302  GGAATATGCTGCTGACATGACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361
Qy      1471  AAAAUGGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1530
Db      362  AAAATGAGAGATGATGATGCTCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
Qy      1531  UUGAGUUGUUGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1590
Db      422  TTAAGATTTGGGATTCAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 481
Qy      1591  CAGGAAACAGAGAAACUGACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1650
Db      482  CAAGAAACGAGAAAGCGACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 541
Qy      1651  CCUGAGUCAGUUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1710
Db      542  CCGAATCAGTGTGTGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 601

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Db      1081 GCTAATGTCTAATTGGGCAAGGGGACGTGTGTTGTAAATGAACGAAAGCTACTT 1140
Qy      2251 AGCAUACUUAUCUGACAGCCAGACAGCAGCAAAAGAUUCGAGCCAUCAU 2304
Db      1141 AGCATCTTAAGTACAGACAGACAGACCAAAAGATTGGATGCGCATCAAT 1194

RESULT 13
US-10-065-133A-25
; Sequence 25, Application US/10065133A
; Publication No. US2003019074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-25

Query Match      38.6%; Score 904.4; DB 13; Length 1194;
Best Local Similarity 64.2%; Pred. No. 3.8e-25;
Matches 767; Conservative 246; Mismatches 181; Indels 0; Gaps 0;

Qy      1111 GAGUACCAUUGUGGAAAGGCAACAGCGUAUACUACAAAAGCAACGAGAGAU 1170
Db      1      GATTACCAATGTGTGGAGAGAGACAGACGCTTCTGAGAAAGCAACCAAGATTG 60
Qy      1171 AUUACAGUCUUAUGUGAGUGAGAGACGAAACGUCGUAUAGCUAGCAUUAUUGGCC 1230
Db      61      ATTCAATTGATGTAAGTGGAGAGATGAACAATCAATTGCGAAGCAATATTGTACC 120
Qy      1231 AUGCUAUUUUCACAAAGAAUUGUAUUAUAAAGCAUUAAGAGUGAUCUUAUUGCGU 1290
Db      121      ATGGTGTTCCTCCAGAAAGATTGCATGTACAAAGAGTTCCAGCGATTGAACCTTCGT 180
Qy      1291 AAUAGGGCAAAUUCAGAGUUGAUAUCCAUUGCAUACUUAUUAAGCATUUUCACAAAGAU 1350
Db      181      AATTAGAGCAAAATCACGCGCTTGAACCCCATGTCACTCTTGAAGCATTTCCAAAAGAT 240
Qy      1351 GCGAAAGUCUUAUUAUUGGAGAAUUGCAAAUUGCAACAAUUGAGUGAGAAUUAU 1410
Db      241      GCAAAAGTGCTTTTCAGAGATTGGGGGAGTGAACCATCGACAATGTATGGAGATGATT 300
Qy      1411 GGGGUUAUACAGACAUAGCUCCAAACACAGAGUUGUAUAGAGGGGUAAAGUCAGC 1470
Db      301      GGAATATTGCTCGATGATGACCCCAAGCAACCGAGATGTCATTGAGAGAGTGAAGTCA 360
Qy      1471 AAAAATGGCGUUAUGAUAUACUCAGCCCGAGAGAGAGUAGUGAGUAGUACCGG 1530
Db      361      AAAATGGAGTGAGTGTAGTACTCCAGACTGAGAGAGTGGTGAGCATTTGACCGTTT 420
Qy      1531 UUGAGAGUUCGAGACCAACGAGAAUUAUACUUAUUCUCUGAGAGAGUCUGAAACA 1590
Db      421      TTAAGAGTTTCGGGATCAAAAGGGAAACATACTACTGTCCCTGAAGAGTCAAGTGAACA 480
Qy      1591 CAGGAGACAGAAACUGAACAAUUAACUUAUCUAGUCGUAUAGUUGGAGAGUUAUUGC 1650
Db      481      CAAGCAGCGAGAAACCTGACATATTTATTCATCATCAATGATGTGGAGATTAAATGCT 540
Qy      1651 CCUGAGUCAGUUGUGCAUUAUCUUAUGAGUAGUAGUAGUAGUAGUAGUAGUAGU 1710

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Db      541      CCGAATCAGTGTGTCTAATCTTATCATGTGATCATAGAACTGGAATTGTGAAA 600
Qy      1711 AUUACAGUUGUCUACAAUCCUACAUUCUUAUUAUAAUUGAUUUGAGCCAUUUCAG 1770
Db      601      ATTCAATGTGTCAAGAGATCCCAACATTTATTAACAATTAAGATTAAGATTGAGCCATTCAG 660
Qy      1771 UCUUAUUGUUCUAAAGGCAUUAAGGCGCAUUAACAGUGUGUUGUUGAGACUUAUUC 1830
Db      661      TCCTGTCTCTAGAGGCACACAGAAAGCCAAATACAGCGGCTTGTGTAACACCTGTCTTTCAG 720
Qy      1831 CAUAUAGAGAGUUAUUGAGAGACUUAUUGAACCCAGCAUUAUUAUAAACUUCUUCUUC 1890
Db      721      CAATTCGAGATGTACTTGAACATTTTATCTGCTCAAAATTAATTAATCTCTCCCTTTT 780
Qy      1891 GCAGCCGCCCCCAACCAAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1950
Db      781      GCGGCTCTCTCTCGGAAACAGAGATGACAGATGCTCTTCTTTGACTGTTAATGTAA 840
Qy      1951 GGAUACGAAUAGAAUUAUUCUUAUAGGGCAUUAUUCUUAUUAUUAUUAUUAUUAUUA 2010
Db      841      GGATCGGAAATGAGGATTAATTGTAAGAGCAATTCCTCACTGTTCAACTAATAAGGCC 900
Qy      2011 ACUAAAGACUAAACAAUUCUGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2070
Db      901      ACTAAGAGCTCAACAGTCTCTGGAAGAAAGATGACAGGTGCTTACTGTAAGACCCAGATGAA 960
Qy      2071 GGCACUUCUGAGUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 2130
Db      961      GGTACGCGCTGAGAGTAATGCTGCTTCTAAGAGGCTTCTCAATTTAGTAAAGAAAC 1020
Qy      2131 AGGAGAUAGAGACCAAGCAUUAUUAAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2190
Db      1021      AAGGATATGTGCGCCAGCACTAAGCATCAATGAAGAACTGAGCAAACTTGCAGAAAGGAGAAA 1080
Qy      2191 GCUAUAUUAUUAUUGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2250
Db      1081      GCTAATGTCTAATTGTGGCAAGGGAGACGTGTGTGTGTAATGAACGAAACGTGACTCT 1140
Qy      2251 AGCAUACUUAUCUGACAGCCAGACAGCAGCAAAAGAUUCGAGUAGGCAUUAU 2304
Db      1141      AGCATCTTAAGTACAGACAGACAGACCAAAAGATTGGATGCGCATCAAT 1194

RESULT 14
US-09-971-372A-15/c
; Sequence 15, Application US/09971372A
; Publication No. US20030035814A1
; GENERAL INFORMATION:
; APPLICANT: Kawaoaka, Yoshihiro
; APPLICANT: Neumann, Gabriele
; TITLE OF INVENTION: Recombinant Influenza viruses for vaccines and gene
; FILE REFERENCE: 960296, 98130
; CURRENT APPLICATION NUMBER: US/09/971, 372A
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: PCT/US00/09021
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/127,912
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)-(12)
; OTHER INFORMATION: BsmBI recognition sequence
; FEATURE:
; NAME/KEY: misc feature

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LOCATION: (18)..(80)
OTHER INFORMATION: Influenza virus sequence
US-09-971-372A-15

Query Match 2.5%; Score 58.2; DB 11; Length 80;
Best Local Similarity 65.1%; Pred. No. 1.8e-06;
Matches 41; Conservative 19; Mismatches 3; Indels 0; Gaps 0;

QY 2279 CCAAAAGAUUCGAGCGCAUCAAUUAUGUGAUAUAGUUUAAAACGACCUUGUUUCU 2338
DB 80 CCAAAAGAUUCGAGCGCAUCAAUUAUGUGAUAUAGUUUAAAACGACCUUGUUUCU 21
QY 2339 ACU 2341
DB 20 ACT 18

RESULT 15

US-09-834-095-19/c
Sequence 19, Application US/09834095
Application No. US20030194694A1

GENERAL INFORMATION:

APPLICANT: Kawacka, Yoshihiro
TITLE OF INVENTION: VIRUSES COMPRISING MUTANT ION CHANNEL PROTEIN
FILE REFERENCE: 800.026051
CURRENT APPLICATION NUMBER: US/09/834,095
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 60/197,209
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 80
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A primer
US-09-834-095-19

Query Match 2.5%; Score 58.2; DB 13; Length 80;
Best Local Similarity 65.1%; Pred. No. 1.8e-06;
Matches 41; Conservative 19; Mismatches 3; Indels 0; Gaps 0;

QY 2279 CCAAAAGAUUCGAGCGCAUCAAUUAUGUGAUAUAGUUUAAAACGACCUUGUUUCU 2338
DB 80 CCAAAAGAUUCGAGCGCAUCAAUUAUGUGAUAUAGUUUAAAACGACCUUGUUUCU 21
QY 2339 ACU 2341
DB 20 ACT 18

Search completed: December 31, 2003, 22:32:22
Job time : 770 secs

[illegible]

Qy	1445	UGUCAUAGACAGCGGUAAGAGUCACAGCAAAUAGCGGUAAGAAUACUCCAGCGGAGCA	1504
Db	994	KKKAKAKARCGCGGGGAAAAAAGRRRAAAARRGAAATAATWAAAAAAGGCGGCGKCKG	1053
Qy	1505	GAGUA 1509	
Db	1054	GAKTA 1058	
RESULT 4			
CNS017KX/C			
LOCUS			
DEFINITION			
CNS017KX 1101 bp DNA linear GSS 26-JUL-1999			
Drosophila melanogaster genome survey sequence Spe end of BAC			
BACN37F10 of DrosBAC library from Drosophila melanogaster (fruit			
fly), genomic survey sequence.			
AL108171			
AL108171.1 GI:5628475			
GSS.			
Drosophila melanogaster (fruit fly)			
Drosophila melanogaster			
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
Ephydroidea; Drosophilidae; Drosophila.			
1 (bases 1 to 1101)			
Genoscope.			
Direct Submission			
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :			
BP 191 91006 EVRY Cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr			
- Web : www.genoscope.cns.fr)			
Determination of this BAC-end sequence was carried out as part of a			
collaboration with the European Drosophila Genome Project (EDGP) -			
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC			
library (Dros BAC) was made by Alain Billaud at CRPH (Centre			
d'Etude du Polymorphisme Humain) with funding provided by a MRC			
project grant. The DNA was prepared from embryos by Alain Bucheton			
and Genevieve Payan. It has been constructed in the vector			
pBelobAC11.			
Location/Qualifiers			
1..1101			
/organism="Drosophila melanogaster"			
/mol_type="genomic DNA"			
/db_xref="taxon:7227"			
/clone="BACN37F10"			
/clone_lib="DrosBAC"			
/plasmid="pBelobAC11"			
/note="end : SP6"			
BASE COUNT			
247 a .84 c 159 g 263 t 348 others			
ORIGIN			
FEATURES			
source			
Query Match 2.1%; Score 48; DB 29; Length 1101;			
Best Local Similarity 16.3%; Pred. No. 3.8;			
Matches 67; Conservative 167; Mismatches 177; Indels 1; Gaps 1;			
Qy	1080	AUUGAAAAUUAAGGUGCAUGAGGUAUUCGAGAUUCACAUUGUGGAAAAAGCGCAC	1139
Db	1076	WKTADKKWTRDUTYDGGGGGGGKKKKGGDRKADYTKDWKGAATRRARMTAATTATATD	1017
Qy	1140	AGCUAUAUCGAAAAACAACACAGAGAUAUGAUUCACUCUAUUGUGUGAGAAGACGA	1199
Db	1016	DTWKRTTGTRTKTRTKWKMWARBAKWBDBWBDTDMWDKMTKWKMDRRTKMTATRGDRA	957
Qy	1200	ACAGUCGUAUGCUGACGAUAUAUUGUGGCCAUGUAUUTUUCACAAGAAGUUGUAUGAU	1258
Db	956	GRARRRDRDRRRRRRRRRTRTKRWRRRAAMWTAMTTWMMGTTKGAMWTKTKRKGGG	897
Qy	1260	AAAGCGAGUAGAGUGUAUCGAUUAUUC-GUUAUAGGCGCAUAUCAGGAUUGAACCCA	1318
Db	896	AAAAADMGRTDWMWDGAAAAAGKDGCKGKARTWGAATAAAAAAAMTKATATGKRRKT	837
Qy	1319	UGCAUCAACUUUUAAGACAUUUUUCAGAAAGUGCGAAAGUUCUUUCAAUAUUGCGGAA	1378
Db	836	TGRAMWAAGRTTMDAATAMTKKRAAAAGRRRAAAAWAKRGTRGGRKKRGTDGDKGT	777

QY	1379	UGGACAAUUCGACAAUGGAGUAGUAGUGGGUUAUUCACAGACUACGACACGA	1438
Db	776	KKKRTTWTCTAAARRRRRAAAAKGTTKKTIGRRARRAMDMWTTTTCGATTRGRGAA	717
QY	1439	CAGACAUUCGCAUUGAGAGGGGUAAGAGUCAGCAAAAUGGCGGUAUGUAUA	1490
Db	716	AAATTGCAAAAATGCTTADAGAAATAAMAWRFTTWDWMAAADAAGAAW	665
RESULT 5			
EX351150/c			
LOCUS			
DEFINITION	EX351150 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens		
ACCESSION	EX351150		
VERSION	EX351150.1 GI:30377590		
KEYWORDS	EST.		
SOURCE			
TAXISM			
	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1089)		
AUTHORS	L.J. W.B., Gruber, C., Jessee, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to technology cluster 8953.f for more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSDBAK019AB05NM1&cluster=8953.f. Contact : Peng liang Email : fliang@life.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSDBAK019AB05NM1.		
FEATURES			
source			
	1..1089		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="CS0DC025YH02"		
	/cissue_type="NEUROBLASTOMA COT 25-NORMALIZED"		
	/cissue_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"		
	/note="First strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
BASE COUNT	219 a 375 c 47 g 446 t		
ORIGIN			
	2.0%; Score 46; DB 13; Length 1089; Best Local Similarity 36.2%; Pred. No. 11; Matches 153; Conservative 41; Mismatches 226; Indels 3; Gaps 1;		
QY	1213	GAAGCAUUAUUGUGCGCAUGGUUAUUUUCACAGAAUGUGUAUAAAGCAGUUGA	1272
Db	1009	GCATTAAGAGAAAGAAAGAGAGATGATGAGAAAAGAAAGATTAAGAAATTAAGTGA	950
QY	1273	GGUGUUCUGAUAUUGGUUAUUAAGCGCAAUUCAGCGCAUUAUCCCAUACAUCUUUA	1332
Db	949	GGAAAGCAATTGTGAGGACTGATGATTTGATGATGGGTTTAAATATTTATGTGTTAAATTA	890
QY	1333	AGACAUAUUCAGAAAGAUUGCGAAAGUGCUUUUCAAUAUUGGGCAUAUUGAACAUUCCAC	1392
Db	889	TAAATTTGTTAGGTACGAAGTCAGAAAGGAGAAAGAAAGAAATGAGATGAGAG	830
QY	1393	AUUGUAGUAGGAU---GAUUGCGGUUAUUCACAGCAUAGCUCCAGACAGACAGAUUGCA	1449
Db	829	CGGGTGTGAAATGCAATGAGCGGATTTTGAATTAATGATATGAGAGAAAAGAGAGAAAG	770

Oy		1450	AUGAGAGGGGAAAGAAGCAGCAAAAUAUUGGGCGCUAUAUUUCACAGCCGAGAGAGUA	1509
Dd		769	AAAGAAGAGGAAAAATGAAGGGGGGAGAGATGAGTGTAGTGATGATTGGATG	710
Oy		1510	GUGUGAGCAUUGACCGGUUUUUUGAGUUGCAGCAACAAGGAAAUUGUACUACUACU	1568
Dd		709	GTGTGAGATGTTGTATGATTAATTAAGTAGTAGGAGAAAGGAGAGTGGGAAAGATAT	650
Oy		1570	CTUGAGAGAGUCAUUGAAACACAGGAAACAGAGAAACUGACAAUAACUACUACUGCA	1629
Dd		649	GAAAGAGAGGAATGCTGTAAGAAAGAAAGAAAGAAAGAAATTTAAATAATATGTACTTA	590
Oy		1630	AUG 1632	
Dd		589	ATG 587	
RESULT 6				
CNS0182P				
LOCUS				
DEFINITION		CNS0182P	1101 bp DNA linear GSS 26-JUL-1999	
ACCESSION			Drosophila melanogaster genome survey sequence Sp6 end of BAC	
VERSION			BACN37D10 of DrosBAC library, from Drosophila melanogaster (fruit	
KEYWORDS			fly), genomic survey sequence.	
SOURCE			AL108811	
ORGANISM			ALI08811.1 GI:5629115	
REFERENCE			GSS.	
TITLE			Drosophila melanogaster (fruit fly)	
JOURNAL			Drosophila melanogaster	
COMMENT			Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
			Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
			Ephydroidea; Drosophilidae; Drosophila.	
			1 (bases 1 to 1101)	
			Genoscope.	
			Direct Submission	
			Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :	
			BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	
			- Web : www.genoscope.cns.fr)	
			Determination of this BAC-end sequence was carried out as part of a	
			collaboration with the European Drosophila Genome Project (EDGP) -	
			http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC	
			library (Dros BAC) was made by Alain Billaud at CEPH (Centre	
			d'Etude du Polymorphisme Humain) with funding provided by a MRC	
			project grant. The DNA was prepared from embryos by Alain Bucheton	
			and Genevieve Payan. It has been constructed in the vector	
			pbeloBAC11.	
FEATURES				
			Location/Qualifiers	
			1..1101	
			/organism="Drosophila melanogaster"	
			/mol_type="genomic DNA"	
			/db_xref="taxon:7227"	
			/clone="BACN37D10"	
			/clone_1lb="DrosBAC"	
			/plasmid="pbeloBAC11"	
			/note="end : SP6"	
			274 a 268 c 128 g 73 t 358 others	
			BASE COUNT	
			ORIGIN	
			Query Match	2.0%; Score 45.8; DB 29; Length 1101;
			Best Local Similarity	12.5%; Pred. No. 12;
			Matches 38; Conservative 149; Mismatches 116; Indels 0; Gaps 0;	
Oy		1043	AGAGAGGGAAGAAAGUCGCGCAUUCUCAAACAUUGAAAUUAGGUGCAGUAGCG	1102
Dd		720	RKKMKGGGCKGAKTKTAAWAKGRKDMGTATAMTWTAADTDTYKAATTDPAKAAACRR	779
Oy		1103	GAUACGAGGCAUUCACAUCAGUUGCGGAAAGGCCAACAGCUAUACUGCAAAACCA	1162
Dd		780	KRDARKTARBOCGRRARRRBRAMAAGCRABADAGARBARAARRAADDDWDMAAAAAAAAA	839
Oy		1163	GGAGAUUGAUUCAGUCUUAUUGUGUGGAGAGACGAAACAGUCGUAUUGCUGAAGCAUUA	1222
Dd		840	AAAAMWTTRWRMDWDMDTRWDODTTTAAWWDARARARRRRRRRRRRRAARRAAD	899

[illegible]

Db		974	RGRKDKORXDGDDDKGKKKKKAkakAKMArTKMWDMDWMDKDMMQSDA.KDRKADDDGA	915
Oy		1176	GCTGATUUGAGUGUGAGAACAACAGUCAGUCAUAUGCTUGAACCAUAUATUUGGCCAUGGU	1239
Db		914	GDCKDGGKGKADDDPTDGTCKDDDDCKKDDPDKAKGTGGDATWMAATDMWMCWADADW	855
Oy		1236	AUUUUCACAAAGAUUUUUAUGAUAAAAGCGUUAGAGUGUAUUCGAUUUUCGUAAUG	1295
Db		854	WTMDAADMDWMADDWMDWAMKMDAMWAGRTADRBDWGDRAGRGGARTRDRKCRADD	795
Oy		1236	GGCANAUCAGCAGCAUUAUCCCAUGCAUCAUCUUUAAGACUUUCGAGAGUAVCGA	1355
Db		794	KRDABDDDBDAATTWTTTTTTTTROTDDMKMTDTTWTKRADRTM-----DRDDDDBRRA	740
Oy		1356	AGUGCUUUUUCAAUAUUGGGAUUUGACAUAUUGACACAUGUGAUGGGAUUUGGUGU	1415
Db		739	GTAGCKMRRTWRKRWRKRDRTDMDDADADFTARDRRRRRGGADAGKKTGRKRRRDR	680
Oy		1416	AUUUACCAAGACUAGUCUCACAGACAGAGUUCUAUGAGAGGGUAAAGUCACCAAAU	1475
Db		679	ATWBRTDWMAADAAMWTTTDTDTDDMPKRDRRKAGARRRRRTTAARAAWMTWRAMPWK	620
Oy		1476	GAGCGUAGAAUUAUUCACAGCGGCGAGUGUGUGUGAGCUUUGACCGCGUUUUGAG	1535
Db		619	WDKTRADRMWRMALDVTTDARKADRWAKRARBARDRRLAAPADRPWTKKITTAT	560
Oy		1536	AGUUCGAGACCACAGAGAAUUGUACUACUUAUCUCUGAGAGGUCAGUGACAACAGGG	1595
Db		559	WTWAARAAMWAMWAMAATTATTTWTTTWWTTTWWTTTWWTTTAAWMAAWMTATWA	500
Oy		1536	AACGAGAAACUGACAUAUACUACUCACUGCGUCAUGAU	1634
Db		499	AMTAAAMAAAAAAATTTTTTTTTTTTTTTWMTAAAWMT	461

RESULT 8
BXJ61080/c LOCUS
DEFINITION BXJ61080 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI079YN16 3-PRIME, mRNA sequence.
ACCESSION BXJ61080
VERSION BXJ61080.1 GI:30374504
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life Technologies, a division of Invitrogen. Contact : Feng liang Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com/ invitrogen Corporation 1600 Faraday Avenue Genosope sequence ID : CSODI079DS08NP1.

FEATURES
source Location/Qualifiers
1..1201
 /mol_isasm="Homo sapiens"
 /db_xref="takon:9606"
 /clone="CSODI079YN16"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT
155 a 152 c 130 g 182 t 582 others

[illegible]

ORIGIN	BASE COUNT	333 a	162 c	148 g	177 t	281 others
Query Match	1.9%;	Score 44.6;	DB 29;	Length 1101;		
Best Local Similarity	21.1%;	Pred. No. 23;				
Matches	82;	Conservative 138;	Mismatches 164;	Indels 5;	Gaps 1;	
Qy	15	AAUUAUUUUCAGUAUUGGAAAGAAUUAUAAAGAAUACGAGUUCUAGUGCGAGUCUGCAC	74			
Db	691	AAAAAAAAAAAAAAAAAARGGGAKAGGGRKAGARAGRGGRGGRARAAAATKTKKTKTKRKA	750			
Qy	75	UCCGCGAGUACUAAACAAAACCAACAGUGG-----ACCAUUAUGCCAUUAUUAAGAAUAC	129			
Db	751	AGRRARRAAAGAAAAAABAAAADAATGTGTAKAAAMRTAAAMKKMDWATDAAAACAABAT	810			
Qy	130	ACAUACAGGAGGCGCAGAGAAAGAACCCGUCACUUAUGAUAGAAUAGUAGCGCAUAGAA	189			
Db	811	RDWTTAAKAKTKTKGAAAATGAWAGAGARBRGRKCKDGTTRARRRAGADGDWDAKAWA	870			
Qy	190	UAUCCGUAUACAGCCGCAAGAGAUACAGAGAUAGUUAUCCUAGAGAGAAUUGACAGGG	249			
Db	871	WAAWAAATTTARWDTATADDDRAAABWKRAAAADADKDKGRARAGGTGRRRRARATRK	930			
Qy	250	CAACUCUUAUGAGUAUAAUAGUGAUGCCGGAUUGGAUUGUGUAGUAGUAUACUCUCUG	309			
Db	931	AKARRRARRAKARRAKKDDAWDGGKKKKDDAAMAAAKGTDGDKKRRARAKTGMKA	990			
Qy	310	GCUGUGACAUUGUGAAUUAUAGAAUUGACCAUAGCAAGUACGUGUACUUAUCCAAAAUUC	369			
Db	991	RADDRRRAAADDDTRMTTKAMWMTDWMATATATDKDTKDRAKKAGKWKTTTTRDRAAKAK	1050			
Qy	370	UACAAACUUAUUUUGAGAAAGUCGAAAG	398			
Db	1051	AKDDTAATRTATATWKAADDRAKARADAYAK	1079			
RESULT 10						
BU771589						
LOCUS	BU771589	833 bp	mRNA	linear	EST 12-FEB-2003	
DEFINITION	SJEDYG01 SJE Schistosoma japonicum cDNA, mRNA sequence.					
ACCESSION	BU771589					
VERSION	BU771589.1	GI:28338905				
KEYWORDS	EST.					
SOURCE	Schistosoma japonicum					
ORGANISM	Schistosoma japonicum					
REFERENCE	Schistosoma japonicum					
AUTHORS	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidae; Schistosomatoidea; Schistosomatidae; Schistosoma.					
	1 (bases 1 to 833)					
	Hu, W., Yan, Q., Shen, D., Liu, F., Xu, X., Zhu, Z., Zhang, X., Wang, J., Sun, J., Xu, X., Wang, Z., Zeng, L., Kong, X., Wu, X., Qu, J., Xu, Z., Huang, J., Ma, Y., Wang, S., Wang, Z., Xue, C., Feng, Z., Chen, Z. and Han, Z.					
TITLE	Expressed sequence tags from eggs of Schistosoma japonicum					
JOURNAL	Unpublished					
COMMENT	Contact: Zeguang Han					
	Chinese National Human Genome Center at Shanghai					
	351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai					
	201203, P. R. China					
	Tel: 86-21-50801919(ex. 45)					
	Fax: 86-21-50801922					
	Email: hanzg@hgc.sh.cn.					
FEATURES	Location/Qualifiers					
source	1. .833					
	/organism="Schistosoma japonicum"					
	/mol_type="mRNA"					
	/db_xref="taxon:6182"					
	/tissue_type="whole egg"					
	/dev_stage="egg"					
	/lab_host="rabbits"					
	/clone_lib="SJE"					
BASE COUNT	334 a	126 c	122 g	251 t		
ORIGIN						

	Query Match	1.9% ; Score 43.8 ; DB 13; Length 833;
	Best Local Similarity	38.5%; Pred. No. 32;
	Matches	92; Conservative 25; Mismatches 122; Indels 0; Gaps 0;
OY	1904 CAAAGCAAGAUGAAGCAGUUCUCUCACUGACUGGUAUGGGGAUCAAGAUCA	1963
Dd	482 CAAGAAAATCATGAAATACAGTTTCGTATCTATTATTAACAATTBGAAGAAAGACAGT	541
OY	1964 GAUACUCGUUAAAGGGCAAUUCUUCCUAUUUACAACAACAAGACCACUAAGACAUAA	2023
Dd	542 CAGGTGTATTCTTATATCTTTTTCTTCACCTCGAAATTCCTTACGAAATAATTAAGCTTA	601
OY	2024 CAUUCUCGGAAGAAGUGCUGCACUUNUACGAAGACCCAGAUAGGCACUUCUGAG	2083
Dd	602 CTACTCTGTGTATATATATATGATTCGCTACTATGTGAAGCATCATTAAGAAAAACGCAAAA	661
OY	2084 UGAGUCGCCUGUCUGACAGAGAUUCCUCAUUCUGGCAAGAGAAUGAGAUUGCA	2142
Dd	662 TAGTCTCTACATATATAGAGAGAGACACTGGGATTAATAAACGATAGTCTTAGCGA	720
P-J-T-11 LOCUS	CNS016E2	1204 bp DNA linear GSS 26-Jul-1999
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC	
KEYWORDS	BACN15A12 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	
VERSION	AL106628	
SOURCE	AL106628.1 GI:5622852	
ORGANISM	GSS. <i>Drosophila melanogaster</i> (fruit fly) <i>Drosophila melanogaster</i> Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Empidoidea; Drosophilidae; Drosophila. 1 (baes 1 to 1204)	
REFERENCE	Genoscope. Direct Submision Submitted (23-Jul-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	
AUTHORS	- Web : www.genoscope.cns.fr	
TITLE	Determination of this BAC-end sequence was carried out as part of a	
JOURNAL	collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.	
COMMENT		
FEATURES	Location/Qualifiers	
source	1..1204	
	/organism="Drosophila melanogaster"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:7227"	
	/clone_lib="BACN15A12"	
	/clone_id="DrosBAC"	
	/plasmid="PbelOBAC11"	
	/note="end : 77"	
BASE COUNT	298 a 172 c 106 g 316 t 312 others	
ORIGIN		
Query Match	1.9% ; Score 43.8 ; DB 29; Length 1204;	
Best Local Similarity	19.8% ; Pred. No. 35;	
Matches	88; Conservative 155; Mismatches 202; Indels 0; Gaps 0;	
OY	1073 UTCACACUUTGAAAUAUAAAGGUGACUGAGGUAUCGAGAGUUCACAAUGGUTUGGAAAA	11322
Dd	1167 WKAIAAAAAAAAAAAAAAAAAKAAADPAAKKKKAAAAAAAAAKAADADAADAAAAAKAVAK	11089
OY	1133 GGCGCACGCUVUACUCGAAAGACACAGAGAGUUCACUUCACUUGUGUGUGUGAA	11922
Dd	1107 AKAAADAAADAAWKKGAABAAAAAARAAAKWKATKDDDDDKDAADBKKKKKAKAKADAD	1048

QY		1193	GAGCGAAGCAGUCGACUACGACAAUAUTUGGGCCAGUCGUUUUUUCAACAAGAUU	1252
Db		1047	KAADKDKKAKADWADDADAADAKKKKKKKKKKDDATDADAARAKKKDKKAKKK	988
QY		1253	GUAGAUAUAAAAGCAUUGAGUGUAUUCGAUUVUUGUAUAVAGGCCAAUUCAGCAUUGA	1312
Db		987	KDKKKAKAKAMKKKKDKKKDKKKKKKKKKKKKKAAAAKAAAAAAAAAKKKDKKKD	928
QY		1313	AUCCAGCAUCAAACUUUUUAAACAUTUUCAAGAAAGAACGAAAGGCUUUUUCAAAAUU	1372
Db		927	AAKAAAKKKKKDAKKKAKKKDDAWAADKAALKKAAKKKKDKKKDAADKKAAADAA	868
QY		1373	GGGGAUUGAACAUUUGCAUUGUGNMGGAAGAUUGGGGUUUUCCAAGCAGUCGUC	1432
Db		867	KKKDKKAAKADKDAKKMKMDKKKKAAPRAAKKGKGGGRKGGAGGGGAAAGATWT	808
QY		1433	CAGCACAGAGAUUCUAUGAGAGGGGUAAAGAGUCACGAAAUUGGGCGUGAGUAUUCU	1492
Db		807	TWAKTDPTTKTAGAGAKTTTCKTTTWATKKGAKKKTBAADKARDKDAATTAKABAA	748
QY		1493	CCAGCGCGAGAGAGUGUGUGAG	1517
Db		747	GAAATKGGGAARAGGAAGXDGAR	723
RESULT 12				
CNS0061A/c				
LOCUS				
DEFINITION				
ACCESION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
BASE COUNT				
ORIGIN				
Query Match				
Best Local Similarity				

Matches 76; Conservative 62; Mismatches 124; Indels 0; Gaps 0;

QY 1354 AAGGCTUUUUUAAAUAUGGGAUUGAACAUUGCAUUGAUUGGGAUUGG 1413
 Db 647 AAGGCGCTTTAAATAAATTTTGTGAAACCGYAYGMYATATTTCCRMAGAA 588
 QY 1414 GUAUUAACAGACAGACUCCAGACAGAGUUGCAUUGAGGGGUAGAAGACAA 1473
 Db 587 TGGGCAHAHABAGSAGAKAATAGMAAABAAAGACMSACMTGCSMTGACASAACT 528
 QY 1474 AUGGCGGUAGUAUUAUUCUCCAGCGGAGAGUAGUAGUAGCAUUGACCGUUUUG 1533
 Db 527 GAGAMTTTMTTAAABACTTTTCMTSCATADGGAAGCTGMAAGSTTTAAASWCA 468
 QY 1534 AGAGUUGAGACAGACAGAAUUGUUCUACUUCUCCUGAGAGUGUAGCAACAG 1593
 Db 467 YTTGCCWCTTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 408
 QY 1594 GGAACAGAGAAACGACAUUA 1615
 Db 407 AATTAAC 386

RESULT 13
 AZ045148/c 204 bp DNA linear GSS 31-JUN-2003
 LOCUS Gm_UMB001_133 G05R UMN Soybean BAC library (PECSBAC4 EcORI) Glycine
 DEFINITION max genomic clone Glycine max genomic clone Gm_UMB001_133_G05,
 genomic survey sequence.
 ACCESSION AZ045148
 VERSION AZ045148.1 GI:7191314
 KEYWORDS GSS.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 204)
 Larson, K., Mudge, J., Cooper, A., Griwna, S., Denny, R., Pennela, S.,
 Danesh, D., and Young, N.D.
 BAC End sequences from a soybean genomic library (UMN)
 JOURNAL Unpublished
 COMMENT Contact: Young Nevin D
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN 55108, USA
 Tel: 612 625 2225
 Fax: 612 625 9728
 Email: nevin@tc.umn.edu
 Sequence on contig Gm_B030_ctg_a near unmapped duplicate of RFLP
 probe pB030. For more information, see Soybase at:
 http://soybase.aron.jastac.edu. please see as an authority for
 the mapping/naming: Cregan P.B., T. Jarvik, A.L. Bush, R.C. G.
 Shoenaker, K.G. Lark, A.L. Kahler, N. Kaya, T.T. Vantosi, D.G.
 Johns, J. Chung, and J.E. Specht. 1999a. An integrated genetic
 linkage map of the soybean genome. Crop Sci. 39:1464-1490
 Seq primer: M13R
 Class: BAC ends.

FEATURES
 source location/Qualifiers
 1..204
 /organism="Glycine max"
 /mol_type="genomic DNA"
 /cultivar="Faribault"
 /db_xref="taxon:3847"
 /clone="Gm_UMB001_133_G05"
 /tissue_type="cotyledon leaves"
 /dev_stage="cotyledon"
 /clone_lib="UMN Soybean BAC library (PECSBAC4 EcORI)
 Glycine max genomic clone"
 /note="Vector: PECSBAC4; The UMN BAC library (Danesh et al
 , Theor. Appl. Genet. 96:196, 1998) was constructed using
 the Eco RI site of PECSBAC4. The library consists of 72

Query Match 1.9%; Score 43.4; DB 28; Length 204;
 Best Local Similarity 38.3%; Pred. No. 29;
 Matches 49; Conservative 25; Mismatches 54; Indels 0; Gaps 0;

QY 1657 UCAGUUGUUGUACUACUACUACUACUACUACUACUACUACUACUACUAC 1716
 Db 183 TAAATGTTATCATCACCACCAATCTTAATACATCATCTTTAAGAAAGCGCTTAATGAG 124
 QY 1717 UGUCUCAGAAUCCUACUACUACUACUACUACUACUACUACUACUACUAC 1776
 Db 123 TGATTTAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 64

QY 1777 GUUCCUAA 1784
 Db 63 TTCCAAA 56

RESULT 14
 BX376097/c 1201 bp mRNA linear EST 08-MAY-2003
 LOCUS BX376097 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CS0DC022YM12 5'-PRIME, mRNA sequence.
 ACCESSION BX376097
 VERSION BX376097.1 GI:30434756
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2866.f
 Contact: Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID : CS0DC022BG060P1.

FEATURES
 source location/Qualifiers
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DC022YM12"
 /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 79 a 152 c 66 g 270 t 634 others
 ORIGIN

Query Match 1.9%; Score 43.4; DB 13; Length 1201;
 Best Local Similarity 8.5%; Pred. No. 44;
 Matches 45; Conservative 224; Mismatches 257; Indels 1; Gaps 1;

QY 3112 UCUGACAGGUGGGAUUGAUAUGACCAUUGACGUGUACUUAUCCAAUAUUA 371
 Db 1074 KRADAAGCGGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1015

